Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli US-09-299-141-9
US-09-299-141-10
US-09-299-141-10
US-09-299-141-11
US-09-299-141-11
US-09-299-141-17
US-09-299-141-17
US-09-299-141-17
US-09-299-141-2
US-09-299-141-2
US-09-299-141-5
US-09-2 υ

US-UT-199-917A-1

Sequence 1, Application US/07789917A

Patent No. 525479

GENERAL INPORATION:

APPLICANT: Srivastava, Arun

TITLE OF INVENTION: SAFE VECTOR FOR GENE THERAPY

NUMBER OF SEQUENCES:

ADDRESSES:
A RESULT 1 US-07-789-917A-1

Gaps ô 100.0%; Score 125; DB 1; Length 145; larity 100.0%; Pred. No. 7e-25; Conservative 0; Mismatches 0; Indels (Query Match Best Local Similarity Matches 125; Conserv

1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60 1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

April 1, 2004, 14:52:43; Search time 53.2407 Seconds (without alignments) 1302.928 Million cell updates/sec

nucleic search, using sw model

OM nucleic

Run on:

US-10-620-039-1_COPY_1_125 125 1 TIGGCCACICCCICITGCG.......CGCAGAGAGAGAGAGACCAA 125 Title: Perfect score: Sequence:

682709 seqs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			æ			SUMMARIES		
Result No.	o H	Score	Query Match	Length	DB	ID	Description	
1	! ! ⊢		100.0	145	-	US-07-789-917A-1	Sequence 1, Appli	
	7	N	100.0	145	m	0	е 4,	
O	m	N	100.0	145	m	-08-525-8	'n	
	4	N	100.0	145	m	-07-982-19	À	
	S	N	100.0	165	Н	US-07-989-841A-1	'n	
	9	125	100.0	165	N		'n	
	7	N	100.0	165	m		Ä	
	œ	CV	100.0	165	4,	US-09-276-625-7	,	
	σ	N	100.0	192	m		m	
	10	N	100.0	4680	-1	-254-358	'n	
	11	N	100.0	4680	Н	US-08-475-391-1	ř	
	12	N	100.0	4680	7	US-08-709-609-1	'n	
	13	N	100.0	4680	ß	PCT-US95-07178-1	Ļ	
	14	a	100.0	5932	4	Ļ	4,	
υ	15	N	100.0	5932	4	US-09-299-141-4	4	
	16	N	100.0	6142	4	-60	ω̈	
ΰ	17	N	100.0	61	4	US-09-299-141-8	ω,	
	18	N	100.0	62	m	US-08-893-327-15	15,	
U	19	N	100.0	62	٣	-08-893-327	15,	
	20	N	100.0	62	M	08-893-327	17,	
υ	21	N	100.0	6280	ო	8-80	17,	
•	22	N		6280	m	US-08-893-327-19	5	
υ	23	N	100.0	6280	m	-08-8	19,	
	24	N	100.0	6565	4	-09-299-141-	, 1,	
υ	25	N	100.0	6565	4	US-09-299-141-1	'n	
	56	125		6714	4	-09-299-141-	ý	
υ	27	125	100.0	6714	4	US-09-299-141-6	ý	

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US-07-982-193-1
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                                                                                                                                                                                                                                                                                   APPLICANT: LATTA, Martine
APPLICANT: LATTA, Martine
APPLICANT: DENEFLE, Patrice
APPLICANT: DENEFLE, Patrice
APPLICANT: VIGNE, Emmanuelle
APPLICANT: VIGNE, Emmanuelle
APPLICANT: VIGNE, Mananuelle
APPLICANT: VIGNE, Mananuelle
TITLE OF INVENTION: INTEGRATIVE RECOMBINANT ADENOVIRUSES,
TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd, 3C43
CITY: Collegeville
STREET: VA
COUNTRY: USA
ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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) LOCATION: 1..145

) OTHER INFORMATION: /note= "Minimal ITR Sequence"

US-08-702-533-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING WATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/02445

FILING DATE: 03-MAR-1994

PRIOR APPLICATION NUMBER: WO PCT/FR95/00233

FILING DATE: 28-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGIGTRATION NUMBER: 38,619

REFERENCE/DOCKET NUMBER: ST94011-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other nucleic acid
                                                                                                                                                                                                                   Sequence 4, Application US/08702573
Patent No. 6033885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 145 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 125; Conservative
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21 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 80
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Sequence 1, Application US/08440738A
Setent No. 586903C
GENERAL INFORMATION:
APPLICANT: Samulski, R. J.
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STRIE: New York
COUNTRY: New York
COUNTRY: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Petentin PC COMPATION:
MEDIUM TYPE: Patentin PC COMPATION:
SOFTWARE: Patentin DATE:
CURREMY APPLICATION DATE:
STILING DATE: MAY 15, 1995
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
TELEPHONE: CALL PENNIE
TELEPHONE: (212) 790-9090
TELEPHONE: CALL PENNIE
TELEPAX: 6121 PENNIE
TELEPAX: 6121 PENNIE
TELEPAX: 6121 PENNIE
SEQUENCE GERRARTICES:
LENGATH: 16 A bese sicient
                                                                                        ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LEUTA A
REGISTRATION NUMBER: 6636-0
REPERENCE/DOCKET NUMBER: 6636-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 125; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TIGGCCACTCCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GCCAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGGGGGACCAAAGGTCGCC 60
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100.0%; Score 125; DB 3; Length 1.
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
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Patent No. 5478745

GENERAL INFORMATION:
APPLICANT: Xiao, X.
TITLE OF INVEXTION: Recombinant Viral Vector System NUMBER OF SEQUENCES:
ADDRESSE: Pennie & Edmonds
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: US.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,193
FILING DATE: 19921125
CLASSITICATION NUMBER: 22,606
REGISTRATION NUMBER: 22,606
REGISTRATION NUMBER: 22,606
REGISTRATION NUMBER: 23,606
REGISTRATION NUMBER: 23,606
REGISTRATION SANS US
TELEFRA: (S16) 742-4343
TELEFRA: (S16) 742-4343
TELEFRA: (S16) 742-4366
TELEFRA: (S16) 742-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,941A
FILING DATE: On even date herewith
                                                                3: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear _
MOLECULE TYPE: DNA (genomic)
ADDRESSES: De STREET: 400 Garue. TTY: Garden City . New York ISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCCAA 125
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US-07-989-841A-1
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PRIOR APPLICATION NUMBER: US 60/086,166
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 165
LYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-702-573-3
US-08-702-573-3
Sequence 3, Application US/08702573
Patent No. 6033885
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 192 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Pou
                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
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                                                                                                                                                                                  1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                 1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAAAGGTCGCC
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                                                                          Query Match
100.0%; Score 125; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Samulski, R.
APPLICANT: Samulski, R.
TITLE OF INVENTION:
FILE REFERENCE:
FILE REFERENCE:
GGS-027
CURRENT APPLICATION NUMBER: US/08/471,914A
CURRENT APPLICATION NUMBER: 08/440,738
RARLIER APPLICATION NUMBER: 08/440,738
RARLIER PILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 13
SOCTHWARE: Patentin Ver. 2.0
SEQ ID NO ILENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09276625
Patent No. 6436392
GENERAL INFORMATION:
APPLICANT: Brgelhardt, John F.
APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 975.007021
CURRENT APPLICATION NUMBER: US/09/276,625
CURRENT FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 125; DB 3;
100.0%; Pred. No. 7e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08471914A Patent No. 6057152
   ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-440-738A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 125; Conservative
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US-09-276-625-7
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-471-914-1
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APPLICANT: LATTA, Martine
APPLICANT: DENEFLE, Patrice
APPLICANT: DENEFLE, Patrice
APPLICANT: VIGNE, Mamanuelle
APPLICANT: PERRICAUDET, Michel
TITLE OF INVENTION: INTEGRATIVE RECOMBINANT ADENOVIRUSES,
TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
                                                                                                                                                                                                                                                                                       21 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGAAAGGTCGCC
                                                                                                                                                                                                                                           1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                                                                                                                                                                     Gaps
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. 6436392 5,478,745
US-09-276-625-7
                                                                                                                                                                                     .;
0
                                                                                                                     Length 165;
                                                                                                                  Query Match
100.0%; Score 125; DB 4; Length 1
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: FR 94/02445
FILING DATE: 03-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00233
FILING DATE: 28-FEB-1995
ATTORNEY/SAENT INFORMATION:
NAME: SMith Ph. D., Julie K.
REGISTRATION NUMBER: 38,619
REPERBRATION TOWNER: 38,619
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd, 3C43
CITY: Collegeville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08475391
Patent No. 5786211
GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Macker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
         Indels
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COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/475,391
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,358
FILING DATE:
FILING BATE:
FILING BATE:
APPLICATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 125; DB 1; ilarity 100.0%; Pred. No. 7.9e-25; Conservative 0; Mismatches 0;
         0; Mismatches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
         Conservative
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 125; Conserv
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         Matches 125;
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US-08-475-391-1
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Pred. No. 7.9e-25;
                                                                                                                                                                                                                                                                                                                                                   Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FRATURE:
NAME/KEY: misc_feature
LOCATION: 1..192
OTHER INFORMATION: /note= "Right ITR Sequence in patent No. 6033885
US-08-702-573-3
                                                                                                                                                                                                                                                                                                                                                Score 125; DB 3;
Pred. No. 7e-25;
; Mismatches 0;
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FILING DATE:
CLASSIPTCATION: 435
CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5658785and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; P:
Matches 125; Conservative 0;
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; MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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TYPE: DNA ORGANISM: Artificial Sequence CRANTER: FRATURE: CHARL INFORMATION: Description of Artificial Sequence:p43C-ATUS-09-299-141-4
                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSITION
APPLICATION NUMBER: PCT/US95/07178
FEILING DATE:
CLASSITION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO:
TELETEX: 25-3856
INFORMATION FOR SEQ ID NO:
CRANATION FOR SEQ ID NO:
TELETEX: 1978-1878
TELETEX: 1978-187
6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: DNA (genomic) PCT-US95-07178-1
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                                                 Chicago
Illinois
                                                                                             STATE: I.
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US-09-299-141-4
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                                                                                                                                                                                                                                                                    Sequence 1, Application US/08709609; Patent No. 585875; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Johnson, Philip R. TITLE OF INVENTION: Methods TITLE OF INVENTION: Methods TITLE OF INVENTION: Methods JOHNSONER ADDRESSE: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Gillo Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COMPUTRY: USA ZIP: G0006; COMPUTRY: READABLE FORM: MEDIUM TYPE: Floppy disk Methods Tower, 2300 COMPUTRY: COMPUTRY: COMPUTRY: COMPUTRY: COMPUTRY: PLOPEY COMPUTRY: COMPUTRY: PLOPEY COMPUTRY COMPUTRY: PLOPEY COMPUTRY 
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TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 125; DB 2;
Best Local Similarity 100.0%; Pred. No. 7.9e-25;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5858775 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMUNICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-709-609-1
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GCCAA 125
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                   121 GCCAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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Best Local Similarity 100.0%; Pred. No. 7.9e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 0
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Sequence 4, Application US/09299141

Patent No. 6461606

GENERAL INFORMATION:
APPLICANT: FLOTTE, TERRICE R.
APPLICANT: SONG, SIHONG
APPLICANT: WORGAN, MICHAEL
TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REPERENCE: 4300.011800
CURRENT APPLICATION NUMBER: 05/09299,141
CURRENT FILING DATE: 1999-04-23
APALIER APPLICATION NUMBER: 60/083,025
RABLIER PELING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 5932
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Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps
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100.0%; Score 125; DB 4; Length 5932;
Best Local Similarity 100.0%; Pred. No. 8e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 0.
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US-09-141-4/C
US-09-141-4/C
Sequence 4, Application US/09299141
Fatent No. 646606
FABURAL INFORMATION:
APPLICANT: FOUTE, TERENCE R.
APPLICANT: BYRNE, BARRY J.
CURRENT APPLICATION WIMBER: US/09/299,141
FILE REFERENCE: 4300.011800
CURRENT FILING DATE: 1999-04-23
EARLIER PILING DATE: 1999-04-24
SALLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 4
LENGTH: 5932
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX384518 Sequence A46401 Sequence	equenc	AXZ86293 sequence K01624 Adeno-assoc	leno-ass	leno-asso sequence	nence	sequenc	BD218219 Adeno-ass	A46400 Sequence 3	AX418199 Sequence	J01902 adeno-assoc	AX135805 Sequence	AX28629Z Sequence AX753252 Sequence	ethod of	J01901 Adeno-assoc	AX262460 Sequence AF043303 Adeno-ass	Sequence	162303 Sequence 1 RD242774 Adeno-ass	BD242775 Adeno-ass	AF028704 Adeno-ass	AK23545/ Sequence AR235457 Sequence	AR235461 Sequence	AR235461 Sequence	AR235454 Sequence	AR235459 Sequence	AR235459 Sequence	AK235462 Sequence	AR235463 Sequence	AR235463 Sequence	AR235464 Sequence	AK235464 Sequence	AR235460 Sequence	AR235456 Sequence			A linear PAT 19-MAR-2002			Parvovirinae; Dependovirus.	cions
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Unclassified.
1 (bases 1 to 145)
Natsoulis,G. and Surosky,R.T.
Targeted nucleotide sequence delivery and integration system
Targeted, 127-7-MAR-2001;
Patent: US 6207457-A 1 27-MAR-2001;
Location/Qualifiers
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/organism="Adeno-associated virus 2"
/molltype="unassigned DNA"
db_xref="taxon:10804"
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Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0;
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Matches 125; Conservative 0; Mismatches 0;
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/organism="unknown"
/mol_type="unassigned DNA"
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Cytotoxic agents
Patent: WO 0180840-A 2 01-NOV-2001;
BTG INTERNATIONAL LIMITED (GB)
Location/Qualifiers
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TITLE
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FEATURES
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AUTHORS
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100.0%; Score 125; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 125; Conservative 0; Mismatches 0;
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Sequence 1 from patent US 6207457.
AR140333.1 GI:14482829
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Sequence 4 from Patent W09523867
Location/Qualifiers
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[2], from KB or HeLa cells.

[2], from KB or HeLa cells.

[3], from KB or HeLa cells.

Both [1] and [2] present the opposite strand from the one presented here. The focus of both papers is the method of replication of the virus. [1] notes that the initial tt is present only 30% of the time; it is shortened to t in 50% of the population and missing altogether in 15% of the population. There is further sequence heterogeneity which can be explained by assuming that the terminal 125 bases, which form an imperfect palindrome, are replaced by their inverted complement during replication. [2] found that deletion of the 9 terminal bases on the right and the 113 terminal bases on the left of AAV 2 genome did not stop DNA replication. Further deletion of either an 11-base symmetrical sequence (bases 89 to 99) in the right terminal repetition inhibits DNA replication. Substitution of either an 8-base (cagactorgo) symmetrical sequence unrelated to the original 11-base sequence restores DNA replication. All of this can be explained by assuming that the 125 base palindrome mentioned above form a t-shaped secondary structure which provides a primer for DNA polymerase during replication.
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Adeno-associated virus 2H
Adeno-associated virus 2H
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Lusby,E., Fife,K.H. and Berns,K.I.
Nucleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
J. Virol. 34 (2), 402-409 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 145)
Lefebvre, R.B., Riva, S. and Berns, K.I.
Conformation takes precedence over sequence in adeno-associated
virus DNA replication
Mol. Cell. Biol. 4 (7), 1416-1419 (1984)
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Adeno-associated virus 2 left terminal sequence.
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'db xref="taxon:10805"
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replication, terminal repeat.
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Matches 125; Conservative 0
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RESULT 6 AA2LTR2

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Original Source text: Adeno-associated virus 2H DNA (clone pSM620 [2]), from KB or HeLa cells.

The focus of both papers is the method of replication of the virus. The focus of both papers is the method of replication of the time; it is shortened to tin 50% of the population and missing altogether in 15% of the population and missing altogether which can be explained by assuming that the terminal 125 bases, which form an imperfect pallindrome, are replaced by their inverted complement during replication. [2] found that deletion of the 9 complement during replication. [2] found that deletion of the 9 complement during replication. Purcher deletion of an 11-base symmetrical sequence (bases 89 to 99) in the right terminal repetition inhibits DNA replication. Purcher deletion of either an 8-base (cagatots) or 12-base (cagatots) symmetrical sequence unrelated to the original 11-base sequence restores DNA replication. All of this can be explained by assuming that the 125 base palindrome mentioned above form a t-shaped secondary structure which provides a primer for DNA polymerase during replication.
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Adeno-associated virus 2H
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Lusby,E., Fife,K.H. and Berns,K.I.
Nucleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
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Lefebvre, R.B., Riva, S. and Berns, K.I.
Conformation takes precedence over sequence in adeno-associated
virus DNA replication
Mol. Cell. Biol. 4 (7), 1416-1419 (1984)
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Adeno-associated virus 2 right terminal sequence.
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/mol type="genomic DNA"
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/db_xref="taxon:10805"
22 bases upstream of HaeIII sites.
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K01625.1 GI:209624
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Matches 125; Conservative 0; Mismatches 0;
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Samulski,R.J. and Xiao,X.
Recombinant viral vector system
Patent: US 5478745-A 1 26-DEC-1995;
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Engelhardt, 7.F. and Duan, D. Adeno-associated virus vectors
Patent: US 6436392-A 7 20-AUG-2002;
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/mol_type="unassigned DNA"
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Sequence 7 from patent US 6436392.
AR223306.1 GI:23331457
 Sequence 1 from patent US 5478745.
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/mol_type="genomic DNA"
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     Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus. 1 (bases 1 to 145)
Berns, K.I., Hauswirth, W.W., Fife, K.H. and Lusby, E. Adeno-associated virus DNA replication Cold Spring Harb. Symp. Quant. Biol. 43 Pt 2, 781-787 (1979) 80023388
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/organism="Adeno-associated virus 2H"
/mol type="genomic DNA"
/db_xref="taxon:10805"

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100.0%; Score 125; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 125; Conservative 0; Mismatches 0;
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Samulski, R. Jude. and Xiao, X.
Recombinant viral vector system
Patent: US 5869305-A 1 09-FEB-1999;
Location/Qualifiers
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Adeno-associated virus 2H
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PAT 26-SEP-2002

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PAT 18-JUN-2002
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Denefle, P., Latta, M., Perricaudet, M. and Vigne, E.
INTEGRATIVE RECOMBINANT ADENOVIRUSES, PREPARATION THEREOF AND
THERAPEUTICAL USES THEREOF
PATENT: WO 9523867-A 3 08-SEP-1995;
RHONE POULENC RORER SA (FR)
Other publication AU 1852695 950918
Other publication AU 1852695 950908.
Location/Qualifiers
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                               100.0%; Score 125; DB 6; Length 1 100.0%; Pred. No. 2.7e-18; ive 0; Mismatches 0; Indels
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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AX418199 1GI:21523203
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Sequence 3 from Patent WO9523867.
A46400.
A46400.1 GI:2300601
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          PAT 30-APR-2001
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28-MAY-2002
20-MAY-1999 JP 2000549752
20-MAY-1999 US 09/276625 PI
F ENGELHARDT, DONGSHENG DUAN, TUYIN YANG
C12N15/00, A01K67/027, A61K31/711, A61K48/00, C07K14/47, C12NS/10, C12N15/00)
C12N5/00
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Location/Qualifiers
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Adeno-associated viruses and uses thereof
Patent: WO 0125465-A 7 12-APR-2001;
University of Iowa Research Foundation (US) ; Engelhardt, John F.
(US) ; Dongsheng, Duan (US) ; Ziying, Yan (US)
Location/Qualifiers
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/organism="unassigned DNA"
/mol_type="unassigned DNA"
/db.rref="tracen:32644"
/noTe="SEQ ID NO:1 of U.S. Patent No. 5,478,745"
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Engelhardt, J.F., Duan, D. and Yang, T.
Adeno-associated virus vectors and uses thereof
Patent: JP 2002515257-A 7 28-MAY-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
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Location/Qualifiers
              DNA

    165
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Sequence 7 from Patent W00125465. AXI06702
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JP 2002515257-A/7.
                                                                                                      AX106702.1 GI:13922363
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Matches 125; Conservative
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                                   DEFINITION
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/mol_type="unassigned DNA"
/db Arzef="laxon:32630"
/note="Inverted terminal repeat from the AAV-2 vector
plasmid pSub 201"
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1. .207
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="synthetic enzyme attachment site sequence"
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100.0%; Score 125; DB 6; Length 198;

Best Local Similarity 100.0%; Pred. No. 2.6e-18;

Matches 125; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 2.6e-18;
tive 0; Mismatches 0; Indels
Patent: WO 0192551-A 1 06-DEC-2001;
UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL (US)
Location/Qualifiers
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Procaryctic libraries and uses
Patent: WO 02066653-A 58 29-AUG-2002;
Xencor (US)
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Sequence 58 from Patent WO02066653.
AX703496.1 GI:29538456
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Matches 125; Conservative
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Secale cereale

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Secale.

1 (bases I to 304)

RS Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J.,

Fenton,R.D., Gustaon,J.P., Han,P.S., Haia,C.C., Kang,Y.,

Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and

Tong,J.C.

The structure and function of the expressed portion of the wheat genomes - Anther CDNA library from rye

Upublished (2000)

Contact: Olin Anderson

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800 Buchanan Street, Albany, CA 94710, USA

Tel: $105595818
BX402654 BX403654
BM807931 AGENCOURT
BH218838 1006008250
BU152072 AGENCOURT
BX403654 BX403654
BX338963 BX338963
CG273564 GGZBB16TH
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GG285957 GGWKG93TH
CG36546 GGZBBO5TH
ALD6742 DYGSGDDFOTH
ALD6742 DYGSGDDFOTH
ALD6742 DYGSGDDFOTH
ALS52621 ALS52621
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BY33594 BX403519
AGG08031 Pan trogl
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BX408476 Pan trogl
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AW727558 GA Ea001
CC778537 ZWMBBCC42
ALZ76477 Tetracdon
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BX338963 BX338963
BX340341 BX403541
BX403541 BX403541
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WHE1260_H03_O062S Secale cereale anther cDNA library Secale cereale cDNA clone WHE1260_H03_O06, mRNA sequence.
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                                 BH218838
BU152072
BX40326963
CG273564
BX338963
CG2753564
BZ532489
BZ53241848
BX4050831
CNS046BO
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       BE495968 WHE1260 H
BZ569259 pacs2-164
AG185368 Pan trog1
BY752719 BY752719
                                                                                                    April 1, 2004, 14:50:59 ; Search time 1603.24 Seconds (without alignments) 2328.267 Million cell updates/sec
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                                                                                                                                                            US-10-620-039-1_COPY_1_125
125
1 TIGGCCACTCCCTCTGCG.......CGCAGAGAGGAGGAGTGGCCAA 125
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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                                                                             nucleic search, using sw model
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gb_est::*
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em_estfun:*
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29.9
29.6
29.6
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Minimum DB seq Maximum DB seq

Database :

Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Score

Result No.

37.8

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us-10-620-039-1_copy_1_125.rst

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hoto="clinical isolate 2-164 Whole genomic shotgun
library.
                                                                                                                                  ch 29.9%; Score 37.4; DB 1 Similarity 56.7%; Pred. No. 61; 68; Conservative 0; Mismatches
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/organism="Pan troglodytes"
/mol_type="denomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector : pBACe3.6
R.Site 1 : ECORI
R.Site 2 : ECORI.
Location/Qualifiers
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                                                                                                                                Query Match
Best Local Similarity
Matches 68; Conserv
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/cullivar="Blanco"
/db xref="texcon:4550"
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/dev_stage="Anther"
/dev_stage="Anther"
/dev_stage="Anther"
/done_lib="Secale Gereale anther CDNA library"
/lone="Vector: Lambda Uni_ZAP XR, excised phagemid;
/note="Vector: Lambda Uni_ZAP XR, excised not boly(A) RNA were prepared (Butler, Ross and Gistafson) at University of Missouri, Columbia. A cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pars2-164 8319.x2r5pl2 pars2-164 Pseudomonas aeruginosa genomic
clone pars2-164 8319, genomic survey sequence.
BZ569259 1 GI:27203589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

(bases 1 to 1015)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
Location/Qualifiers
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Fax: 2066857244
Email: craymond@u.washington.edu
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/strain="2-164"
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                                                                                          PEATURES
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ORIGIN

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2. (bases 1 to 1049)

SES Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Hattori, M., and Sakaki, Y.
Direct Submission

Licet Submission

AL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Turrumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                            Pan troglodytes DNA, clone: RP43-059G23.TJ, genomic survey sequence.
AG185368 , AG185368.T GI:16715048
GSS.
Pan troglodytes (chimpanzee)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                      4 GCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
                                                                                                                                                                                                               4 GCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
                                                        Gaps
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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Length 1015;
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                                                     Indels
  DB 28;
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source
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AUTHORS
TITLE
JOURNAL
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BX403654
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Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 644)

Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kayosawa, H.; Yagai, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Kayosawa, H.; Yagai, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Kayosawa, H.; Yagi, K.; Tomaru, Y.; Baldarelli, R.; Hilli, D.; Bult, C.; Gojobori, T.; Baldarelli, R.; Hilli, D.; Bult, C.; Crobani, L. E.; Cousine, S.; Dalla, E.; Dragani, T.A.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.; Garibodid, M.; Gissi, C.; Godzik, A.; Godgi, J.; Grimmond, S.; Hirokawa, N.; Jackson, I.J.; Jarvis, E.D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Lee, Y.; Lenhard, B.; Lomis, P.; Maltais, L.; Marchhomi, L.; McKennie, I.; Miki, H.; Nagashima, T.; Ravasi, T.; Pavan, W.J.; Pertea, G.; Pesole, G.; Ravasi, T.; Reed, J.C.; Reed, D.J.; Reid, J.; Rig, B.L.; Konita, M.; Sandellin, A.; Schneider, C.; Semple, C.A.; Setou, M.; Shimada, K.; Sandai, T.A.; Schneider, C.; Wang, Y.; Maranabe, Y.; Wanger, L.; Wanser, M.; Yang, I.; Yang, I.; Yang, I.; Yang, I.; Wanger, L.; Wanser, M.; Yang, I.; Hayatsu, N.; Hirozane-Kishikawa, T.; Zavolan, M.; Zahu, Y.; Aswai, J.; Asawa, K.; Shinagawa, T.; Rukud, S.; Hara, A.; Hashizume, M.; Matambe, Y.; Matane, M.; Sato, K.; Shinaka, T.; Rukud, S.; Hara, A.; Hashizume, M.; Matane, M.; Yasunishi, A.; Yasunishi, A.; Yasaki, X.; Sasaki, D.; Sabaki, S.; Analgawa, A.; Yasunishi, A.; Sasaki, Y.; Analgawa, M.; Yasunishi, A.; Yasunishi, A.; Yasaki, Y.; Waterston, R.; Rogers, J.; Bittney, B. and Hayashizaki, Y.

Nature 420, 563-573 (2002)
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 18-18-18-145-503-9226
Fax: 81-45-503-9226
Fax: Ranome-resegneriken.go.jp/
Adachi, J., Azawa, K., Akimura, T., Azakawa, T., Kawai, J., Kojima, Y., Ructani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, Y., Tagami, M., Piccat, Subaki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                           644 bp mRNA linear EST 17-DEC-2002 BY75219 RIKEN full-length enriched, adult inner ear Mus musculus EX75219
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                           BY752719.1 GI:27183756
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PUBMED
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AUTHORS
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JOURNAL TITLE

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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library denome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Brail: Sequencage - Centre National de Sequencage
Email: Sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invircogen. Contact : Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invircogen.com/ Invircogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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1 (bases 1 to 1103)

1 'A.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stāgē="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
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tissue_type="inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geogracia de la consecución del consecución de la consecución de l
                                                                    Zea mays
Zea mays
Lea mays
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCCACTCCCTCTCTGCGCCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
18 GCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGC
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Frax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 COCCCOGGCTTTGCCCCGGCCGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAG
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Pred, No. 2e+02;
                                                                                                                                                                                                                      875 CCGGGCCGCCTCCGTGCCGCGCGCGCGTGGCGCGCTGCC 919
                                                                                                                                                               78 CCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGAGGGAGTGGC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: transposon-tagged.
Location/Qualifiers
1. 595
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1 Similarity 56.5%;
65; Conservative
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Matches 65; Conserv
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone=lib="NHH_MGC_41"
/note="Organ: skin; Vector: poTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GCCACAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Buperseript II RT (Life Technologies). Note: this is a
NHH_MGC Library."
                                    /tissue type="PLACENTA"

/close lib="Homo sapiens PLACENTA"

/close lib="Homo sapiens PLACENTA"

/note="Wetor: pMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer of the not loned into
the Not I and EcoRV site gested with Not I and cloned into
the Not I and EcoRV site of the pCMVSPORT 6 vector.
Library was not normalized."
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57, mENA Sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Email: cgapbs-r@mail.nh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1981 row: o column: 11
High quality sequence stop: 290.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1103;
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Pred. No. 1.9e+02;
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1 Similarity 11.7%; Pred. No. 1.9e-
13; Conservative 68; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:5472226"
clone="CL0BA007ZH12"
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FEATURES

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(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="FIACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EccRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
E 1 (bases 1 to 1103)
S. Liw. B., Cauber. C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
L Unpublished (2001)
Contact: Genescope
Contact: Genescope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqrefégenoscope.ons.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Introgen. Contact: Feng Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA007ZH12FP1.

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1 (Dases 1 to 530)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B/3 Maize Seedlings and Silks Unpulished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
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G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@lastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM079047 530 bp mRNA linear EST 14-NOV-
MEST88-F06.T3 ISUM4-TN Zea mays CDNA clone MEST88-F06 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA007ZH12"
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BX403654 EXA03654.1 GI:30762430
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8749018 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6334507
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/db_xref="taxon:1000"
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/lab host="#HIOB (phage-resistant)"
/lab host="#hIOB (phage-resistant)"
/lone="forgan: ofocysts; Vector: pcMV-SPORT6.1; Site 1:
/note="forgan: ofocysts; Vector: pcMV-SPORT6.1; Site 1:
/note="forgan: ofocysts; Vector: pcMV-SPORT6.1; Site 1:
/note: forgan: ofocysts; Vector: pcMV-SPORT6.1; Site 1:
/note: forgan: ofocysts; Vector: pcMV-SPORT6.1; Site 1:
/note: forgan: 
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence start: 3
High quality sequence start: 3
Location/Qualifiers
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Pred. No. 2.2e+02;
); Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                        3U152072.1 GI:22665604
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VERSION KEYWORDS SOURCE ORGANISM

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Tel: 301-838-5843
Fax: 301-838-0208
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CG273564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resulting DNA:RNA hybrid was treated with RNAse H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT713PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO65DH04QP1:
Location/Qualifiers
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BX338963.1 GI:30347036
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1 (bases 1 to 514)

1 (Jam. B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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as spacers.
PCR PRimers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
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larity 55.9%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                      CTA TAG)
SACKWARD: Backward PCR primer sequence, primer T3
TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
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/lab host="DH108"
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/clone="MEST88-F06"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
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/cultivar="B73"
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CG2BB16TH ZM 0.7 1.5 KB Zea mays genomic clone ZMWEMa0750D08, genomic survey sequence.
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1 (basea I to 598)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Reenick,A., Fraser,C.M., Budiman,M.A., Badell,J.A., Rohlfing,T., Cirek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                    64
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CS0D1065YP0R"
/clone="ICS0D1065YP0R"
/clone_Tib="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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/mol_type="genomic DNA"
/grain="B73"
/clone="ZAMBMBM0750D08"
/clone="IASMBM 073.5 KB"
/clone="IASMBM 073.5 KB"
/molylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                     27.7%; Score 34.6; DB 13; Length 514; 28.9%; Pred. No. 2.4e+02; ive 43; Mismatches 43; Indels 0.
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/organism="Zea mays"
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Seg primer: Tk
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CG285957 AM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0607P17, genomic survey sequence. CG285957.1 GI:34200171
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Marze Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-6208
Fax: 301-838-6208
Email: whitelaw@tigr.org
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Whitelaw(C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Umpublished (2002)
Other_GSSs: OGWKG93TV
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27.7%; Score 34.6; DB 28; Length
Best Local Similarity 59.8%; Pred. No. 2.6e+02;
Matches 58; Conservative 0; Mismatches 39; Indels
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Class: sheared ends.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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BZ410270 GI:26042544 GSS.
                                                                                                                                                                                                                                                                                BZ532489 654 bp DNA linear GSS 16-DEC-2002 OGAEY44TC ZM2_0.7_1.5_KB Zea mays genomic clone ZMMBMa0046G15, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
( Dades l to 634)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Coltek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
         169 GTGAGCTTGGTGAGGCACTTGAGCCGGGCAACCTCCGCCAGTATGGAGCACGAGATGGC 228
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Tel: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-5843
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1. 654
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/porganism="zea mays"
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/db xrefe="texon-4577"
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/clone="ZMYBMA0046GIS"
/clone="Location SMYBMA0046GIS"
/clone="Location
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methylation filtered genomic DNA library"
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Query Match 27.7%; Score 34.6; DB 29; Length 827; Best Local Similarity 59.8%; Pred. No. 2.7e+02; Matches 58; Conservative 0; Mismatches 39; Indels 0;

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Search completed: April 1, 2004, 17:02:17 Job time : 1606.24 secs

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ALI3360B Tetracdon
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BX405071 BX405071
BX50571564 OGDABBUTC
CG273564 OGDABBUTC
CG285957 OGMAGDUTC
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AX017628 MUS muscu
BH218838 100608250
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Silurana tropicalis
Silurana tropicalis
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana
I bases 1 to 974)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela (1239)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheda, MD 20892
Bldg. 31 Rml0A07 Betheda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
CDNA Library Preparation: Wei Wu, DKF2
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT 15918074 XtSt10-30 Silurana tropicalis cDNA clone IMAGE:7027270 3', mRNA Sequence.
CF784470
CF784470.1 GI:37748315
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      BY752719
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AUTHORS
TITLE
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          CF784470 AGENCOURT
BE495968 WHB1260 H
BZ569259 pacs2-164
AG185368 Pan trogl
                                                                                                                                        1, 2004, 14:50:59 ; Search time 1859.76 Seconds
(without alignments)
2328.267 Million cell updates/sec
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145
1 TIGGCCACTCCCTCTCTGCG......CTCCATCACTAGGGGTTCCT
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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BE495968
BZ569259
AG185368
                                                                                                       nucleic search, using sw model
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em gss inv: *
em gss yln: *
em gss vrt: *
em gss fun: *
em gss mus: *
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gb_gssl: *
gb_gss2: *
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Maximum DB seq length: 2000000000
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Database :

Result Š.

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EST 20-0CT-2003

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ch 26.1%;
l Similarity 57.9%;
66; Conservative
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                                                                                                                                                                                                                                /done="trakonisas" / done="trakonisas" / done="vector: pkkw2: Site_1: BamHI; Site_2: XhoI; 10 ug / note="vector: pkkw2: Site_1: BamHI; Site_2: XhoI; 10 ug of poly4+ RNA was isolated from a mixture of embryos at stage 10. 20 and primed by oligo-dr primer: S-GAGAGAGGAAGGATCC(T)16VN-3' (where v=g,h,C).
5-methyl-dcTP was used instead of dcTP in the first-strand synthesis in order to get heminmethylated cDNA. After full:length enrichment, oligo-dg tailing and normalization against itself; second-strand synthesis was carried out by priming with 5'-GAGAGAGAGACTGGAGTAATTAATC(3)3-3' dsDNA was digested with XhoI/BamHI and directionally cloned into the pkkw2 vector. Average insert size is 1:8 b. Library constructed using the Carninci protocol (Genome Research 2000) by Drs. W. Wu and C. Niehrs (DKFZ, Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 bp mRNA linear EST 02-AUG-2000 CDNA clone WHE1260, H03_0062S Secale cereale anther cDNA library Secale cereale BE495968 WHE1260_H03_006, mRNA sequence.
BE495968.1 GI:9662561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secale cereale (rye)
Secale cereale
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Secale.
I (Dases: 1 to 304)
Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J.,
Penton,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y.,
Penton,R.D., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM14761 row: d column: 20
High quality sequence start: 36
High quality sequence stop: 157.
Location/Qualifiers
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                                                                                                                                               1. .974
/organism="Silurana tropicalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 26.6%; Score 38.6; D Similarity 91.1%; Pred. No. 35; 41; Conservative 0; Mismatches
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/wol_type="mRNA"
                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:8364"
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BE495968/c
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/dr.xref="txxxxx:4550"
/clone="WHBI260 H03 OO6"
/clone="WHBI260 H03 OO6"
/tissue_type="Adult plant before anthesis"
/dov.stage="Adult plant before anthesis"
/dov.stage="Adult plant before anther cDNA library"
/clone_lib="Secale carbod bul-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/inte="Vector: Lambda Uni-ZAP XR, excised phagemid;
/inte="Vector: Lambda Uni-ZAP XR, excised phagemid;
/inte and the me prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TD Close lab (Choi, Close, Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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1015 bp DNA linear GSS 17-DEC-2002
pacs2-164_8319.x2r5p12 pacs2-164 Pseudomonas aeruginosa genomic
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1 (Dassa; 1 to 1015)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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/strain="2-164"
/db_xref="taxon:287"
/clone="paca2-164_8319"
/clone lib="paca2-164_8319"
/note="clinical isolate 2-164 Whole genomic shotgun
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Pred. No. 68;
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Location/Qualifiers
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BZ569259.1 GI:27203589
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Direct Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpesegencriken:go:jp, URL:http://hgp.gsc.riken.go:jp/,
Tel:81-45-503-9111, Fax:81-45-50-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                  noidosos 1049 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-059G23.TJ, genomic survey
sequence.
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Pan.
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Toroki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
Unpublished
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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52; Indels
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
db_xref="texon:9598"
/clone="RP43-059G23.TJ"
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ON BYTSTID RITER full-length enriched, adult inner ear Mis musculus CDDA Clone F330101F05 5', mRNA sequence. Adult in the control of MYSSTID GITSTA3756

S. MST. and could thouse mouse)

INSTRUCTION OF GITSTA3756

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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.

(S. 11, W. B., Gruber, C., Jessee, J. and Polayes, D.

Eni, W. B., Gruber, C., Jessee, J. and Polayes, D.

Dupublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12914687.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 seqrefagenoscope. Cns.fr, Web: www.genoscope.cns.fr

Email: seqrefagenoscope. Cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2860.r For
more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODMO14DE06NP1&cluster=2860.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
Library Avenue Genoscope sequence ID: CSODMO14DE06NP1.

Location/Qualifiers

Location/Qualifiers
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                  prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                             /dev_stāgē="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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Experimental Animal Research in Riken contributed
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1 Similarity 56.1%; Pred. No. 92;
69; Conservative 0; Mismatches
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/dev_stage="fetal"
                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                  |db|xref="taxon:10090"
|c1one="F930013F16"
|tissue_type="inner ear"
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/db_xref="taxon:9606"
/clone="CS0DM014YJ12"
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Lusubude 1121 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 603C03 of library B from Tetraodon nigroviridis, genomic survey sequence of the contraction of th
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/clone lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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AL336088.1 GI:8229846
SS. genome survey sequence.

"Etraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Teleostei; Buteleostei; Neoteleostei;
Acauthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/mol_type="genomic DNA"
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14.0%; Pred. No. 1.2e+02;
ive 66; Mismatches 51;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191006 EVRY cedex - France
BP 191006 EVRY cedex - France
BMail: seqrefâgenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10245.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOAG006BD03NP1&cluster=10245.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAG006BD03NP1.
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/coll_line="RAWOS CELL LINE)"
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CG273564
CG273564.1 GI:34185705
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BX405071 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
CLONE CSODG006YG06 3-PRIME, mRNA sequence.
BX405071
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1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone="Ci0BA07ZH12"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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1 (bases 1 to 1103)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulliength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBAOO7ZH12FP1.
/clone="003C03"
/clone lib="B"
/note="Genoscope sequence ID : C0AB003AB02C1~end : T?"
                                                                                                                                                                                                                                                                                                                                                                                         4 GCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGA
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                                                                                                                                                                                                               Length 1121;
                                                                                                                                                                                                                                                                                                           72; Indels
                                                                                                                                                                                                          Score 35.8; DB 29;
Pred. No. 1.7e+02;
0; Mismatches 72;
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l Similarity 47.1%;
64; Conservative
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.XB Zea mays genomic clone ZMMBMa0020023,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Freser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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/clone="ZnwBwa0046G15"
/clone="be-cr. pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

/ And type="genomic DNA"
/ strain= B73"
/ db xref="texon:4577"
/ clone="ZMVBMa0020023"
/ clone="ZMVBMa0020023"
/ clone="Ib=-ZM, 71.5 kB"
/ note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 hethylation filtered genomic DNA library"
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TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
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organism="Zea mays"
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genomic survey sequence.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
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(Dases 1 to 654)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunber, C.M., Budiman, M.A., Bedall, J.A., Roblfing, T., Consortium for Maize Genomics
                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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/note="Vector: pBcSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Email: whitelaw@tigr.org
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/strain="B73"
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Contact: Cathy Whitelaw
TIGR
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CG441848 840 bp DNA linear GSS 17-SEP-2003 OG3DB09TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0779B18, genomic survey sequence.
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1 (bases 1 to 840)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSS: OG19809TV
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methylation filtered genomic DNA library"
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712 Medical Center Drive, Rockville, MD 20850, USA 712 Medical Center Drive, Rockville, MD 20850, USA 712: 301-838-508
Email: whitelaw@tigr.org
Seq primer: TR
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9712 Medical Center Drive, Rockville, MD 20850, USA
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/mol_type="genomic DNA"
/strain="B73"
    Consortium for Maize Genomics
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CG441848.1 GI:34820478
GSS.
                        Unpublished (2002)
Other GSSs: OG2BF05TV
Contact: Cathy Whitelaw
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Best Local Similarity 57.85
The Gal Conservative
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OG2BP05TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0751B10,
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(Dases 1 to 827)
Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunber, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGMKG93TV
Other GSSs: OGMKG93TV
Other GSSs: Cathy Whitelaw
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1 (bases 1 to 839)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
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/strain="B3"
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/clone="ZNMBMa0607P17"
/clone="Jb="ZN 0.7 1.5 KB"
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    533 CTGGGCGCCACCATTGAGAGCTCGAGCTCCTTGAGAGCCTGCATCCGAC 485
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1 Similarity 57.8%; Pred. No. 1.98+02;
63; Conservative 0; Mismatches 46; Indels 0;
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9712 Medical Center Drive, Rockville, MD 20850, USA
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/organism="Zea mays"
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Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Query Match Best Local S: Matches 63

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS

RESULT 14 CG365468

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Search completed: April 1, 2004, 17:02:14 Job time : 1875.76 secs

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Sequence 1, Appliance 2, Appliance 2, Appliance 1, Applia
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Sequence 6, Application US/09782378A

Sequence 6, Application US/09782378A

Patent No. US20020102731A1

GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bandalon, Ziv
APPLICANT: Gandalon, Ziv
APPLICANT: Gandalon, Ziv
APPLICANT: Gandenko, Dmitri
TITLE REPERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A

CURRENT FILING DATE: 2001-02-12

PRIOR FILING DATE: 2000-10-02

NUMBER: OF SEQ ID NOS: 27

SEQ ID NO 6

LENGTHALE: PATENTIN NOS: 27

SEQ ID NO 6

LENGTHALE APPLICATION NUMBER: MOVERNOR SEQ ID NO 6

SEQ ID NO 6

LENGTHALE APPLICATION NUMBER: MOVERNOR SEQ ID NO 6

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LENGTHALE APPLICATION NUMBER: MOVERN
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             ORGANISM: Homo sapiens
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Sequence 8, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 58, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 33, Appli
Sequence 32, Appli
                                                                                                                                                                                                                               April 1, 2004, 16:04:14; Search time 218.574 Seconds (without alignments) 2480.895 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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145
1 TTGGCCACTCCCTCTGCG.......CTCCATCACTAGGGGTTCCT 145
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-782-378A-8
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US-10-159-968-13
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US-10-159-968-13
US-10-159-968-13
US-10-159-985-416-33
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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US-10-159-968-13/c

US-10-159-968-13/c

Sequence 13, Application US/10159968

PUDLICATION NO. US2003015294A1

GENERAL INFORMATION:
APPLICANT: Manatov, Serge

TITLE OF INVENTION: Defective Viral Vectors That are Helper Free

TITLE OF INVENTION: Defective Viral Vectors That are Helper Free

FILE REPERBYCE: 600-1-286

CURRENT FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: US 60/294,797

PRIOR APPLICATION NUMBER: US 60/294,797

PRIOR FILING DATE: 2001-08-07

PRIOR FILING DATE: 2001-08-07

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH 164
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                                                                                                                                                                                                                                                                              Sequence 7, Application US/10054665

Publication No. US20020197237A1

GENERAL INFORMATION:

APPLICANT: Engelhardt, John F.

APPLICANT: Duan, Dongsheng

TITLE OF INVENTION: Adeno-associated virus vectors

FILE REFERENCE: 875.007US2

CURRENT APPLICATION NUMBER: US/10/054,665

CURRENT FILING DATE: 2002-06-13

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 145; DB 13;
100.0%; Pred. No. 1.6e-32;
tive 0; Mismatches 0;
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                                 121 GCCAACTCCATCACTAGGGGTTCCT 145
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CRGANISM: Adeno-associated virus
US-10-159-968-13
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Matches 145; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 165
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US-10-054-665-7
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RESULT 2
US-10-135-984-8
; Sequence 8, Application US/10135984
; Sequence 10. US20020182595A1
; Publication No. US20020182595A1
; GENERAL INFORMATION:
    APPLICANT: Matchew D. Weitzman
; APPLICANT: Anton J. Cathomen
; TITLE OF INVENTION: REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
; TITLE OF INVENTION: REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
; FILE REPERBNCE: SALKINS.041A
; CURRENT FILING DATE: 2002-08-05
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 146
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100.0%; Score 145; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.66-32;
Matches 145; Conservative 0; Mismatches 0; Indels
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Sequence 8, Application US/09782378A;
Patent No. US20020102731A1
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Banbou, Wadie
APPLICANT: Gartenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SEGVEWARE: Patentin Version 3.0
SEQ ID NOS: 27
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; ORGANIEM: adeno-associated virus
US-10-135-984-8
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ORGANISM: Homo sapiens
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US-09-782-378A-8
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; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. US20020197237A1 5,478,745
US-10-054-665-7
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DE142
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,777
PRIOR APPLICATION NUMBER: 60/200,777
PRIOR APPLICATION NUMBER: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 955
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Publication No. US2030171312A1
GENERAL INFORMATION:
APPLICANT: XIAO, XIAO
TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DE1142
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                                                                                                                                                                                                                                                                                                        Length 207;
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 58
; LENGTH: 207
; TYPE: DNA
; PRANTSM: Artificial sequence
; FRATURE:
; OTHER INDORMATION: synthetic enzyme attachment site sequence
US-10-023-208-58
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ilarity 100.0%; Pred. No. 1.2e-32;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     100.0%; Score 145; DB 14;
100.0%; Pred. No. 1.5e-32;
ive 0; Mismatches 0;
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Publication No. US20030171312A1
GENERAL INFORMATION:
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Matches 145; Conservative
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COCGANISM: Homo sapiens
US-09-845-416-26
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Matches 145; Conserv
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US-09-845-416-26
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US-10-276-356-1
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US-10-276-356-1/C
US-10-276-356-1/C
Sequence 1, Application US/10276356
Publication No. US20040029106A1
GENERAL INFORMATION:
APPLICANT: University of No. US20040029106A1th Carolina at Chapel Hill
APPLICANT: Samulski, R. Jude
APPLICANT: McCarty, Douglas M.
TITLE OF INVENTION: DUPLEXED PARVOVIRUS VECTORS
FILE REPRENCE: 5470-282
CURRENT APPLICATION NUMBER: US/10/276,356
CURRENT FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
LENGTH: 175
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                                                Length 165;
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Publication No. US20030124537A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Wan-Ching
TITLE OF INVENTION: PROCARYOUT LIBRARIES AND USES
FILE REFERENCE: A.70174.1/RFT/RMS/RWK
CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT FILING DATE: 2001-12-17
PRIOR PILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 63
                                                DB 14;
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Pred. No. 1.6e-32;
; Mismatches 0;
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                                             100.0%; Score 145; DB 14; 100.0%; Pred. No. 1.6e-32; ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pi
Matches 145; Conservative 0;
                                                                                al Similarity 100.
145; Conservative
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US-10-023-208-58
                                             Query Match
Best Local S
Matches 145
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Query Match
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US-09-845-416-33
; Sequence 33, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
; APPLICANT: XIAO, XIAO
; TITLE OF INVENTION: DAN SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
; TITLE OF INVENTION: THEREOF
; FILE REPRENCE: DE1142
; CURRENT APPLICATION NUMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,777
; RIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOOFWARE: Patentin Ver. 2.1
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100.0%; Score 145; DB 10; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 955;
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CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,777
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 955
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US-09-845-416-26
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LENGTH: 987
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Sequence 33, Application US/09845416; Publication No. US20030171312A1; GENERAL INFORMATION:

RESULT 11 US-09-845-416-33/c

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987 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGGGGACCAAAGGTCGCC 928
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US-09-845-416-32
US-09-845-416-32
US-09-845-416-32
| Sequence 32, Application US/09845416
| Publication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICANT: XIAO, XIAO
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| CURRENT APPLICATION NUMBER: US/09/845,416
| CURRENT PILING DATE: 2001-04-30
| PRIOR PILING DATE: 2001-04-28
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 32
| MANDER APALET AP
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE TITLE OF INVENTION: THEREOF ENCODING A DYSTROPHY MINIGENE AND USE FILE REFERENCE: DELIA.

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT FILING DATE: 2001-04-30

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

LENGTH: 987
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100.0%; Pred. No. 9.8
:ive 0; Mismatches
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US-09-845-416-32/c
; Sequence 32, Application US/09845416
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Matches 145; Conservative
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CORGANISM: Homo sapiens
US-09-845-416-33
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ORGANISM: Homo sapiens
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4414 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAGGTCGCC 4355
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| Sequence 31. Application US/09845416
| Publication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICANT XIAO, XIAO
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REPRESENCE: DB1142
| CURRENT APPLICATION NUMBER: US/09/845,416
| CURRENT PILING DATE: 2001-04-30
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 36
| SEQ ID NO 31
| LENGTH: 4476
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE TITLE OF INVENTION: THEREOF FILE REPRENCE: DE1142
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT APPLICATION NUMBER: US/09/845,416
PRIOR APPLICATION NUMBER: 02001-04-30
PRIOR FILING DATE: 2000-04-28
SUGUREN OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
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ORGANISM: Homo sapiens
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Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT: XIAO,

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION WHOBER: US/09/845,416

CURRENT APPLICATION NUMBER: 60/200,777

PRIOR APPLICATION NUMBER: 60/200,777

PRIOR APPLICATION UNMER: 2000-04-26

NUMBER OF SEQ ID NOS: 36

SOFUMARE: Patentin Ver. 2.1

SEQ ID NO 31

LENGTH: 4476
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Job time : 229.574 secs
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; ORGANISM: Homo sapiens
US-09-845-416-31
RESULT 15
JS-09-845-416-31/c
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1090s:* geneseqn2000s:* geneseqn2001ss:* geneseqn2001ss:* geneseqn2002s:* geneseqn2003ss:* geneseqn2003ss:* geneseqn2003bs:* N Geneseq 29Jan04:* 1: geneseqn1980s:* geneseqn2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Acf35877	Aaq41448	Aat03385	Aat63408	Aax34295	Aba02990	Abs69884	Acc58491	Acf35876	Abx93568	Aaq66769	Aat 49462	Aad03535	Abs69886	Abv77279	Aat03384	Η.	Aad37254	Aad37254	Aad37261	Aad37261	Aad37260	Aad37260
SUMMARIES	ID	ACF35877	AAQ41448	AAT03385	AAT63408	AAX34295	ABA02990	ABS69884	ACC58491	ACF35876	ABX93568	AAQ66769	AAT49462	AAD03535	ABS69886	ABV77279	AAT03384	AAD44621	AAD37254	AAD37254	AAD37261	AAD37261	AAD37260	AAD37260
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	Length	144	145	145	145	145	145	145	145	145	146	165	165	165	165	165	192	207	955	955	987	987	4414	4414
dł	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125
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AAD37259 AAD37259 AAD37258 AAD37258	AAH41481 AAF89931 ABA02989 ABS69879	ABS69880 ADE76508 AAI66974 AAF23750 ABK89694	AAEV76133 AAT09008 ABX14497 ADA50070 AAF23749	AAD37257 AAD37263
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ALIGNMENTS

Adenovirus; Rep78; Rep68; CAP; gene therapy; AAV-2; ITR; ds. AAV-2 right inverted terminal repeat sequence. ACF35877 standard; DNA; 144 BP. 17-JAN-2003; 2003WO-US001624. 18-JAN-2002; 2002US-0349532P. (first entry) Adeno associated virus. WPI; 2003-627412/59. (UYDU-) UNIV DUKE. WO2003061582-A2. Zhang X; 31-JUL-2003. 06-NOV-2003 ACF35877; Li C, RESULT 1 ACF35877

New recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed, useful as a vector for gene therapy.

Example; Page 120; 122pp; English.

The invention relates to a recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed. A complete virus-mediated system for recombinant AAV production is provided which comprises: (a) a first recombinant adenovirus encoding one or more AAV REP78/68 polypeptides and one or more AAV REP78/68 polypeptides and one or more a gene of interest and AAV inverted terminal repeats that flank the gene of interest; (c) vital helper functions; and (d) a host cell comprising the first recombinant adenovirus, the second recombinant adenovirus, and the vital helper functions. The recombinant adenovirus, and the vital helper functions. The recombinant AAV is useful as a vector for gene therapy. The present sequence represents an AAV-2 right inverted terminal repeat (ITR) sequence

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inverted terminal repeats. The vector is safe for use in gene therapy, partic. in treatment of haemoglobinopathies and a variety of diseases, e.g. thalassemia, diabetes, sickle cell anaemia, and cancer. See also AAQ41449. (Updated on 25-MAR-2003 to correct PN field.)
                                                  Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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                                                                                                               Adeno-associated virus-2 basal vectors - for gene therapy and treatment of haemoglobinopathies and cancer etc. - has cassette contg. a promoter capable of cell-specific expression, between 2 inverted terminal repeats of the adeno-associated virus 2.
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                                                                                          79
                                                                                                                                                                                                                                                                                                                         Adeno-associated virus 2; ITR; site-specífic íntegration; vector; cell-specífic; gene therapy; haemoglobinopathies; thalassemia; diabetes; sickle cell anaemia; cancer; parvovirus; B19; ss.
                                                                                            CTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                                    Gaps
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                                 Length 144;
                                                    Indels
           A; 49 C; 52 G; 20 T; 0 U; 0 Other;
                              .Match
Local Similarity 100.0%; Pred. No. 1.2e-23;
les 125; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                 BP
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(first entry)
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            Sequence 144 BP; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inverted terminal repeat, ITR; adenovirus, adeno-associated virus; AAV-2; replication defective; integration; gene therapy; ds.
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                                                                                                                                                                                                                                 Recombinant defective adenovirus contg. integratable expression casset - for use in gene therapy to express protein, antigen or antissense nucleic acid, also for prodn. of recombinant adeno-associated viruses.
                                                                                                               TTGGCCACTCCCTCTGTGCGCGCTCGCTCACTGAGGCCGGGCGAACGTCGCC
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Score 125; DB 2;
Pred. No. 1.2e-23;
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   Ouery Match 100.0%; Score 125; Dest Local Similarity 100.0%; Pred. No. 1.2 Best Local Similarity 100.0%; Mismatches 125; Conservative 0; Mismatches
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18-APR-1996
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                                                                                                    1 rrescentrecererentes de la respectación de la res
                                                                      1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                         Gaps
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          Length 145;
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          Score 125; DB 2;
Pred. No. 1.2e-23;
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note= "region C"
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'note= "region D"
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Query Match
Best Local Similarity 100.0
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The present sequence is the inverted terminal repeat (ITR) from the wild type adeno associated virus (AAV) serotype 2 genome. A novel nucleic acid construct, comprises a targetting sequence capable of binding AAV Rep, or 1 the present sequence, and at least 1 heterologous nucleotide sequence arranged relative to the targetting sequence, so that it is integrated into a target site in a recipient genome. The integration cystem can be used to integrate a selected nucleotide sequence into a recipient cell genome, useful in the treatment of an acquired or inherited disease, e.g. long term gene therapy. The integration system can be size specific integration characteristics of AAV, is not limiting in regard to the size of the nucleotide sequences into the recipient cell genome. Specifically it can be used to safely and efficiently cell genome specifically it can be used to safely and efficiently recipient cell genome without the risk of causing insertional mutagenesis cellibration events
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Pred. No. 1.2e-23;
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100.0%; Score 125; D
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 125; Conservative 0; Mismatches
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Natsoulis G, Surosky RT;
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                                                                    WPI; 1997-192917/17
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20-APR-2000; 2000GB-00009887.

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associated virus (AAV) vectors comprising a promoter e.g. an AAV promoter (AAX34296) and a selected DNA sequence, especially an AAV rep gene and a parvovirus B19 cap gene, located between 2 AAV inverted terminal repeats (ITR) such as the ITR sequence shown here. The system can specifically target primitive progenitor and differentiated cells of the erythroid genes. The vectors can be used for the in vitro or in vivo delivery of genes to cells such as bone marrow cells, peripheral blood cells, endothelial cells and myocardial cells
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                                                                                                                                                                                                                                                                                                                                                                Cytostatic; virucide; apoptosis inducer; p53; Saos-2 cell; infection; cancer; virus; HPV16; HPV18; adeno-associated virus 2; AAV-2; ss.
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                                                                                                                                                                                                                                                                                       100.0%; Score 125; DB 2; Length 145; 100.0%; Pred. No. 1.2e-23; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                Seguence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                          The invention relates to new recombinant chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus 2 ITR SEQ ID NO 2.
                                                                          New recombinant adeno-associated vectors
(ADRE-) ADVANCED RES & TECHNOLOGY INST.
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/note= "unpaired base"
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/note= "unpaired base"
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1. .145
                                                                                                 Claim 2; Page 69; 76pp; English.
                      Srivastava A, Ponnazhagan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-GB001795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA02990 standard; DNA; 145
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/label= ITR
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(first entry)
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Best Local Similarity 100.
Matches 125; Conservative
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The invention relates to single stranded and/or looped DNA having a portion with at least one base, internally located with respect to any 3' and 5' ends of the DNA, that is unbasepaired with another base in a form that is capable of being internalised within a target cell, for use in therapy, with cytostatic and virucide activity. The DNA acts as an application in cells that lack p53 functionality, useful for application preferably a dividing cell where the cell is other than a sasociated with a solicit where the peptide or protein that selectively kills the cell. The DNA is preferably in the form of an AAV or associated with AAV protein which has been treated such that the DNA is no longer capable of replication or expression in cells and is associated with or contained within a vehicle which is associated with or contained within a vehicle which is associated cancer into a target cell. The DNA is also useful for manufacturing a medicament for treating an individual suffering from a mutant p53 associated cancer can infection that inhibits cellular b53. The method targets cancer cells infected with p53 inhibiting viruses, such as HPV16 or HPV18 and only cells that lack p53 activity are killed and no damage to cellular DNA is involved. The present sequence is that of the adenosassociated virus (AAV) 2 ITR, the double loop structure found at each end of the AAV DNA. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector, adenovirus, adeno-associated, adenosine deaminase gene, receptor, adenosine deaminase deficiency; severe combined immune deficiency; PAH, beta-chain, haemoglobin gene, beta-thalassaemia, sickle cell disease, low density lipoprotein gene, familial hypercholesterolaemia, hypoxanthine-guanine phosphoribosyltransferase, Lesch-Nyhan syndrome; phosphoribosyltransferase, inesch-Nyhan syndrome; gene therapy; phenylketonuria, dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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                                                                                                                                                                          Single stranded and/or looped DNA for treating mutant p53 associated cancer or infection that inhibit cellular p53, having portion with an base, internally located with respect to any 3' and 5' ends of the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 145 BP; 24 A; 49 C; 52 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 125; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      Example 11; Page 38; 51pp; English.
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                                           (BTGI-) BIG INT LID
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                                                                                       Beard PM;
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                                                                                       Rај К,
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Producing an adeno-associated virus (AAV) in an insect cell, e.g. for gene therapy, comprises introducing an insect cell-compatible vector into an insect cell and maintaining the insect cell under conditions that
                                                                                                                   AAV; inverted terminal repeat; insect; gene therapy; vector; ss.
                                                                     Adeno associated virus inverted terminal repeat region.
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                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2001; 2001US-00986618.
13-AUG-2002; 2002US-00216870.
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                       (first entry)
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/*tag= a
                                                                                                                                                                 Adeno associated virus.
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                       26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5' and 3' end, left and right inverted terminal repeats of adenovirus flanking NS, adenovirus packaging sequence linked to inverted terminal repeat, and adeno-associated virus terminal repeat linked to 3' end of NS, into cell expressing adenovirus early gene lacking from vector and culturing cell to produce another vector. The method is useful for generating vectors, especially mAd vectors. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo. The nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deficiency with severe combined immune deficiency, beta-chain of disease associated with beta-thalassaemia and sickle cell disease, receptor for low density lipoprotein gene associated with familial hypercholesterolaemia, hypoxanthine-guanine phosphoriansferase associated with lesch-Myhan syndrome, phosphoriansferase associated with lesch-Myhan syndrome, dystrophin gene associated with muscular dystrophy, and human cystic dibrosis. Transmenbrane conductance regulator gene associated with cystic fibrosis transmenbrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adenosassociated virus 2 (AAV2) terminal repeat sequence that was used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing vector, by introducing vector having nucleotide sequence, adenovirus inverted terminal repeats and packaging sequence, and adenoassociated virus terminal repeat, into cell, and culturing cell.
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antianaemic; antilipaemic; nootropic; cytostatic; dermatological;
human adeno-associated virus 2; AAV2; terminal repeat; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                            Sandalon Z, Gnatenko DV;
                                                                                                                                                                                                                                                                                                           (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 191pp; English.
                                                                                                                                                                                                               12-FEB-2001; 2001US-00782378.
                                                                                                                                                                                                                                                             2000US-0237747P.
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                                                                                                                                                                                                                                                                                                                                                            Hearing P, Bahou WF,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-690619/74.
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                                                                                                                   US2002102731-A1.
                                                                       Homo sapiens.
                                                                                                                                                                                                                                                             02-OCT-2000;
                                                                                                                                                                 01-AUG-2002
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The present sequence is that of an adeno associated virus (AAV) palindromic inverted terminal repeat (ITR) region. An AAV ITR is used in novel insect cell-compatible vectors of the invention that are designed for the production of AAV in insect cells. The vectors comprise an AAV ITR and coding sequences for AAV VP1, VP2 and VP3 capsid proteins, for AAV non-structural replication (Rep) proteins Rep52 or Rep40, and for AAV Rep78 or Rep68. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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0
                                                                                                                                                                                                                                                                                                                                                                                 Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 145 BP; 23 A; 49 C; 52 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 125; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV-2 left inverted terminal repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACF35876 standard; DNA; 145
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ID ACE3
XX
AC ACE3
XX
DT 06-N
XX
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ACC58491 standard; DNA; 145 BP.

RESULT 8
ACC58491/c
ID ACC5/XX
AX
AC ACC5/

ACC58491;

GCCAA 125

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misc_binding
 The invention relates to a recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed. A complete virus-mediated system for recombinant AAV production is provided which comprises: (a) a first recombinant adenovirus encoding one or more AAV REP78/68 polypeptides and one or more ABV REP78/68 polypeptides and one or more agene of interest and AAV inverted terminal repeats that flank the gene of interest; (c) viral helper functions; and (d) a host cell comprising the first recombinant adenovirus, the second recombinant adenovirus, and the viral helper functions. The recombinant adenovirus, and the viral helper functions. The recombinant AAV is useful as a vector for gene therapy. The present sequence represents an AAV-2 left inverted terminal repeat (ITR) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                       wew recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed, useful as a vector for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treeccactcccrcrcrececectcecrcecrcacteaeeccacaagercecc
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
            Adenovirus; Rep78; Rep68; CAP; gene therapy; AAV-2; ITR;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus-2 inverted terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 125; DB 8;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                         Example; Page 120; 122pp; English.
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                                                                                            17-JAN-2003; 2003WO-US001624
                                                                                                                 18-JAN-2002; 2002US-0349532P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inverted terminal repeat; viral regulatory element.
                                Adeno associated virus
                                                                                                                                                                             WPI; 2003-627412/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GCCAA 125
                                                                                                                                    (UYDU-) UNIV DUKE
                                                    WO2003061582-A2
                                                                                                                                                        Zhang X;
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                                                                       31-JUL-2003
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The invention relates to identifying molecules that interact with an aden-associated viral regulatory element (e.g.a Rep recognition sequence, RSD comprising contacting at least one molecule with a nucleic sequence, RSD comprising contacting at least one molecule is bound to the viral regulatory elements. Also included is a kit for analysing the interaction between molecules and an adeno-associated viral regulatory element. The method is useful for identifying molecules e.g. at least one cellular protein, recombinant proteins, synthetic protein or exogenous protein (preferably human proteins that are derived from a cDNA library or cellular lysate), or peptide, antibody, nucleic acid, lipid, carbohydrate and/or organic or inorganic compound that interacts with an adeno-associated viral regulatory element comprising an inverted terminal repeat (ITR) or regals or the method broadens the understanding of adeno-associated virus (AAV) and facilitates the application of adeno-associated virus-based vector system, therefore ITR-binding proteins and other molecules provide new insights into the AAV life cycle, including the regulation of gene expression and integration, and suggests improvements for its application in thereapy. The present is an AAV-2 ITR containing an RRS used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of cellular regulations of adeno-associated virus involves contacting an adeno-associated viral regulatory interacting molecule with a nucleic acid comprising a adeno-associated viral regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= f bbound molecty= "Nucleotides 41-1 of the present sequence" 33,\ .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13"
1. .41
/*tsg= a
/bound_moiety= "Nucleotides 125-85 of the present
                                                                                                                                                                                                                                                 '4. .62
*tag= c
'bound_molety= "Nucleotides 50-42 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= e
/bound moiety= "Nucleotides 72-64 of the present
                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/bound_moiety= "Nucleotides 84-76 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= g
/label= Rep_recognition_sequence
/label= This RRS is specifically claim in claim
122. .127
                                                                                                                                                                                   "Nucleotides 62-54 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= h
'label= Terminal_resolution_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 16pp; English.
                                                                                                                                                    /*tag= b
/bound_moiety= "
sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-2001; 2001US-0286951P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weitzman MD, Cathomen AJ;
                                                                                                                                                                                                                                                                                                                                                      sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WEIT/) WEITZMAN M
(CATH/) CATHOMEN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002182595-A1
                                                                                                                     misc_binding
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/*tag= m
/label= Double-D
/label= Double-D
/label= This 165 bp sequence, resulting from addition of
a second D repeat to the AAV ITR, has not been identified
in any naturally occurring virus!!
1. .145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type= INVERTED
/label= D_repeat
21. .145
/*tag= 1
/label= T-shaped
/note= "The naturally occurring 145 bp ITR sequence can
form a T-shaped structure for DNA replication when single
                        /*tag= .c
/rpt_type= INVERTED
/label= A/_repeat
/note= "Forms the stem of a T-shaped structure when base
paired with repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type= INVERTED
/standard_name= "ITR"
/note= "This naturally occurring 145 bp ITR is located
both ends of the AAV genome"
1. .20
/*tag= b
                                                                                                                                                                                                                                                         Adeno associated virus inverted terminal repeat with double D region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= j
/note= "Part of T-shaped structure, formed by base
paring between the C' and C repeats"
63. .70
/*pt type= INVERTED
/label= C'_repeat
74. .81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= **
//*tag= **
//*tag= **
//*tag= "Part of T-shaped structure, formed by base paring between the B' and B repeats"
//*tag= f
                                                                                                                                                                                                                                                                                     Viral replication; REP protein; inverted terminal repeat; ITR; adeno-associated virus; AAV; vector; double-D; cis-acting; lytic life cycle; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _dg= e
/rpt_type= INVERTED
/label= C_repeat
*tar
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                AAT49462 standard; DNA; 165 BP.
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                               associated virus.
                                                           121 GCCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_structure
                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                            10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_unit
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                                                                                                                                                                                                                                                                                                                                                               Synthetic.
   61
                                                                                                                                                                                             AAT49462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stem_loop
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                                                                                                                                                                                                                                                                                                                                                 Adeno
                                                                                                                                     RESULT 12
                                                                                                                                                   AAT49462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The 20-bp D-sequence given in AAQ66773 is present in the inverted terminal repeat (ITR) sequence of AAV and is required for viral replication. A novel, modified terminal repeat structure, double-D ITR, was constructed (AAQ66769) that contained a single 145 bp ITR sequence with an additional D' sequence. The double-D ITR fragment allows proficing including double-D ITR can be used for gene replacement therapies. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                   TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double-D ITR; inverted terminal repeat; D-sequence; AAV; adeno-associated virus; capsid; encapsidation; gene therapy; vector; ds.
                                                                                        1 TIGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenovirus associated viral inverted terminal repeat - for use in recombinant viral vector system for treatment of genetic diseases.
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                           100.0%; Score 125; DB 7; Length 146;
.larity 100.0%; Pred. No. 1.2e-23;
Conservative 0; Mismatches 0; Indels
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Seguence 146 BP; 21 A; 53 C; 49 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 25; 44pp; English
                                                                                                                                                                                                                                                                                                                 AAQ66769 standard; DNA; 165 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00989841.
                                                                                                                                                                                                                                                                                                                                                                                                                         Double-D ITR terminal repeat.
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                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samulski RJ, Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-217868/26.
                                           Similarity
                                                                                                                                                                                                             GCCAA 125
                                                                                                                                                                                                                                        GCCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9413788-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-1992;
                                              Best Local Simi
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
20-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                               AAQ66769;
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                            Query Match
                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                  AAQ66769
ID AAQ6
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à g inverted terminal repeat double DD DNA sequence

WO200125465-A1.

12-APR-2001.

Unidentified

19-JUN-2001 (first entry)

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Recombinant adeno-associated virus; rAAV; circular intermediate; ITR; inverted terminal repeat; haemostatic; antisickling; neuroprotective; antianaemic; noortopic; blood disorder; sickle cell anaemia; thalassaemia; neurological disorder; haemophilia; Alzheimer's disease; muscle disorder; Parkinson's disease; gene delivery; erythropoietin; epo; CFTR; cystic fibrosis transmembrane conductance receptor; tyrosine hydroxylase; glucocerebrosidase gene; Gaucher's disease; gene therapy; Double DD; ds.
                                     AAD03535 standard; DNA; 165
                                                                 AAD03535;
              RESULT 13
                           AAD0353
                                        The adeno associated virus (AAV) has a 145 bp inverted terminal repeat (ITR) located at each end of its genome. In addition to being able to base pair with each other. The ITRs can also individually fold back on the part of the part of the ITRs can also individually fold back on the mealves through the base pairing of A, A', B, B' and C, C' sequences to form a T-shaped structure for DNA replication (See features table). It has been found that viral mutants with deleted D sequences are unable to replicate their DNA. Addition of a second D repeat (D') to the naturally occurring ITR resulted in a sequence, designated double-D, which was sufficient to carry out the functions normally required of two wild-type irrs during a lytic AAV viral infection, i.e. it is capable of directing replication and assembly into AAV, and/or the integration into the host genome, of recombinant DNA containing the mucleic acid molecule. Vectors and viral particles containing the double-D sequence are useful in gene therapy. Replication and integration into the host genome is completely effected through the double-D sequences, ensuring that the heterologous
                                                                                                  /rpt_type= INVERTED
/label= A repeat
/note= "Forms the stem of a T-shaped structure when base
paired with A' repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                             Double-D sequence directs adeno-associated virus integration into host genome - used in gene therapy, maintains full length coding sequence of therapeutic gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 TIGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 125; DB 2;
100.0%; Pred. No., 1.2e-23;
iive 0; Mismatches 0;
                                                                                                                                                                        /*tag= i
/label= D'
/note= "Additional D' sequence"
                                       /*tag= g
/rpt_type= INVERTED
/label= B'_repeat
104. .145
'rpt_type= INVERTED
'label= B_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 9; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%;
Matches 125; Conservative (
                                                                                                                                                                                                                                                                                  96WO-US006786
                                                                                                                                                                                                                                                                                                            95US-00440738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene sequences remain intact
                                                                                                                                                              .165
                        96. .103
                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                       (SAMU/) SAMULSKI R J. (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                Samulski RJ, Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-042643/04.
                                                                                                                                                                                                                               WO9636364-A1
                                                                                                                                                                                                                                                                                   14-MAY-1996;
                                                                                                                                                                                                                                                                                                            15-MAY-1995;
                                                                                                                                                                                                                                                        21-NOV-1996
                           repeat_unit
                                                                              repeat_unit
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The patent discloses a composition comprising at least two recombinant adeno-associated viruses (rAAVs). Each rAAV contains a recombinant DNA and condecule comprising three DNA segments linked together. The first and the third DNA segments comprises 5' and 3' inverted terminal repeats (ITRs) respectively from the circular intermediate of AAV. The second DNA segment in each virus is different and does not comprise AAV sequence. It preferably comprises sequences encoding a therapeutically effective polypeptide such as the cystic fibrosis transmembrane conductance receptor gene (CTRR), the erythropoietin (epo) gene, the tyrosine hydroxylase gene (Parkinson's syndrome) or the glucocear- brosidase gene (Aducher's disease). The circular intermediate of AAV imparts increased episomal stability and persistence of the vector in the host cell. Compositions comprising TAAV sequences are useful for transferring recombinant vector is useful in medical therapy, which includes the recombinant vector is useful in medical therapy, which includes treatment or prophylaxis of blood disorders involving skeletal, cardiac or smooth muscle Adv vector is used as a delivery vehicle for gene therapy. The present sequence is the ITR DD DNA sequence referred to as "doubbe sequence". This sequence is the ITR DD DNA sequence referred to 5',478,745. This sequence is not used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for transferring recombinant DNAs and to express a polypeptide in a host cell, comprises two recombinant adeno-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                       Dongsheng D, Ziying Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 139; 144pp; English.
                                                                             07-OCT-1999; 99US-0158209P.
06-OCT-2000; 2000WO-US027863
                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
(ENGE/) ENGELHARDT J F.
(DONG/) DONGSHENG D.
(ZIYI/) ZIYING Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-266321/27.
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                                                                                                                                                                                                                                                                                                                                                                                       Engelhardt JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim
Matches 125;
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GCCAA 125 GCCAA 145

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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5 and 3 end, left and right inverted terminal repeats of adenovirus flanking NS, adenovirus packaging sequence linked to inverted terminal repeat of adenovirus flanking S. denovirus packaging sequence linked to inverted terminal repeat linked to inverted the delicity sequences and inverted terminal vectors, especially mad vectors. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase deficiency with severe combined immune deficiency, beta-chain of the emerglobin gene associated with beta-thalassemia and sickle cell disease, receptor for low density lipoprotein gene associated with hypercholesterolaemia, hypoxanthine-guanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain, haemoglobin gene; beta-thalasseamia; sickle cell disease; low density lipoprotein gene; beta-thalasseamia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; phenylalamine hydroxylase gene; gene therapy; phenylkenouvia; phenylalamine hydroxylase gene; gene therapy; phenylkenouvia; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antianaemic; antilipaemic; nootropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds.
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                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing vector, by introducing vector having nucleotide sequence, adenovirus inverted terminal repeats and packaging sequence, and adenoassociated virus terminal repeat, into cell, and culturing cell.
  TIGGCCACICCCICITCIGCGCGCCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
                                        21 Trasccacrecererensesserreseresereateasessassesses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adeno-associated virus 2 terminal repeat DD sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sandalon Z, Gnatenko DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 8; 191pp; English
                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000; 2000US-0237747P.
                                                                                                                                                                                                                                                                                                                                       ABS69886 standard; DNA; 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-690619/74.
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                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                            phosphoribosyltransferase associated with Lesch-Nyhan syndrome, hencylalanine hydroxylase (PAH) gene associated with phenylketonuria, dystrophin gene associated with muscular dystrophi, and human cystic fibrosis transmembrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adeno-associated virus 2 (AAV2) terminal repeat sequence that was used in the methods of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of pTRT, a circular adeno-associated virus
                                                                                                                                                          ; Score 125; DB 6; Length 165; ; Pred. No. 1.2e-23; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Circular adeno-associated virus; CAAV; replication; hairpin;
                                                                                                                                Sequence 165 BP; 24 A; 59 C; 53 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 27 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 53; 69pp; English.
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Matches 125; Conservative 0
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1 TIGGCCACTCCCTCTGCG......CGCAGAGAGGGAGTGGCCAA 125
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Description	Sequence 1, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 13, Appl	Sequence 1, Appli	ŝ	Sequence 26, Appl	Sequence 26, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 32, Appl	Sequence 32, Appl
EI.	US-09-928-158B-1	US-09-782-378A-6	US-10-240-198-2	US-10-135-984-8	US-09-782-378A-8	US-10-054-665-7	US-10-159-968-13	US-10-276-356-1	US-10-023-208-58	US-09-845-416-26	US-09-845-416-26	US-09-845-416-33	US-09-845-416-33	US-09-845-416-32	US-09-845-416-32
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1	ALIGNMENTS 928158B ION COMPETENT AAV HELPER 5-06 0 0 0	100.0%; Score 125; DB 9; Length 130; Conservative 10.0%; Pred. No. 1.4e-25; Conservative 0; Mismatches 0; Indels 0; Gaps ITTGGCCACTCCTCTGGGGCTGGCTGCTCACTGAGGGGGGACCAAAGGTGGCGTTGCCGGGGGACCAAAGGTCGCCGGGGGGGG
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	tion US/09 77222A1 LI LI REPLICAT 2 REPLICAT 2 REPLICAT 2 NUMBER: 2 2002-0 NUMBER: 0 008-1 0 05: 9 version 3	larity 100.0% Conservative (CONSTITUTE) CONSTITUTE (CONSTITUTE) CONSTITUTE (CONSTITUTE) (CONSTIT
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TITLE OF INVENTION: MEGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
FILE REFERENCE: SALINIS.041A
CURRENT APPLICATION NUMBER: US/10/135,984
CURRENT APPLICATION NUMBER: 60/286951
PRIOR FILING DATE: 2001-04-27
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO
Query Match 100.0%; Score 125; DB 14; Length 145; Best Local Similarity 100.0%; Pred. No. 1.3e-25; Matches 125; Conservative 0; Mismatches 0; Indels 0.
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APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Gratenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONNES-04970
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 66/237,747
PRIOR APPLICATION NUMBER: 66/237,747
PRIOR APPLICATION NUMBER: 66/237,747
SOFTWARE: PATENTING SOO-10-02
NUMBER OF SEO ID NOS: 27
SOFTWARE: PatentIn version 3.0
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; ORGANISM: adeno-associated virus
US-10-135-984-8
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US-09-782-378A-8
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100.0%; Pred. No. 1.3e-25;
cive 0; Mismatches 0;
                     Sequence (Application US/09782378A Patent No. US20020102731A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Banchou, Wadie
APPLICANT: Gandenko, Dmitri
APPLICANT: Gantenko, Dmitri
APPLICANT: Gantenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFRENCE: STONYB-04970
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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Publication No. US20030100115A1
GENERAL INFORMATION:
APPLICANT: BTG INTERNATION:
APPLICANT: BTG INTERNATION:
APPLICANT: BTG INTERNATION:
TITLE OF INVENTION: CYTOTOXIC AGENTS
FILE REFERENCE: 142184WO
CURRENT APPLICATION NUMBER: US/10/240,198
CURRENT APPLICATION NUMBER: 0009987.1
PRIOR APPLICATION NUMBER: 0009987.1
PRIOR APPLICATION NUMBER: 0009987.1
PRIOR APPLICATION NUMBER: 0009987.1
PRIOR FILING DATE: 2000-04-20
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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; LOCATION: (94)
COTHER INFORMATION: Unpaired base
US-10-240-198-2
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LOCATION: (72)
OTHER INFORMATION: Unpaired base
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Best Local Similarity 100.
Matches 125; Conservative
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OTHER INFORMATION: ITR
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US-09-782-378A-6
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LENGTH: 145
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US-10-054-665-7
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                                                                                                Query Match
100.0%; Score 125; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 125; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7. Application US/10054665
Fublication No. US20020197237A1
GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Dian, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.001082
CURRENT APPLICATION NUMBER: US/10/054,665
CURRENT FILING DATE: 2002-06-13
FRIOR APPLICATION NUMBER: US 09/276,625
FRIOR APPLICATION NUMBER: US 00/086,166
FRIOR FILING DATE: 1999-03-25
FRIOR APPLICATION NUMBER: US 00/086,166
NUMBER OF SEQ ID NOS: 13
SEQ ID NOS: 13
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Publication No. US20030152914A1
GENERAL INFORMATION:
APPLICANT: Kaplitt, Michael G.
APPLICANT: Musatov, Serge
: TITLE OF INVENTION: Method for Generating Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                   1 TTGGCCACTCCCT
; SEQ ID NO 8
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-378A-8
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ORGANISM: Unknown
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US-10-159-968-13/c
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; FEATURE:
1 OTHER INFORMATION: Inverted terminal repeat from the AAV-2 vector plasmid pSub 201
US-10-276-356-1
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| Publication No. US20040029106A1
| Publication No. US20040029106A1
| Publication No. US20040029106A1th Carolina at Chapel Hill
| PublicANT: University of No. US20040029106A1th Carolina at Chapel Hill
| APPLICANT: Samulski, R. Jude
| APPLICANT: Samulski, R. Jude
| APPLICANT: McCarty, Douglas M. |
| TITLE OF INVENTION: DUPLEXED PREVOVIRUS VECTORS |
| FILE REFERENCE: 5470-282 |
| CURRENT FILING DATE: 2001-05-31 |
| PRIOR PILING DATE: 2001-05-31 |
| SOFTWARE: Patentin Version 3.1 |
| SEQ ID NOS: 1 |
| SED ID N
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TITLE OF INVENTION: Defective Viral Vectors That are Helper Free
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                               FILE REFERENCE: 600-1-286
CURRENT APPLICATION NUMBER: US/10/159,968
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/294,797
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PASLESE for Windows Version 4.0
SEGITHAL: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA CRENO-associated virus US-10-159-968-13
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us-10-620-039-1_copy_1_125.rnpb

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Query Match
Best Local Similarity 100.0%; Pred. No. 8.8e-26;
Matches 125; Conservative 0; Mismatches 0;
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; Sequence 33, Application US/09845416
; Publication No. US20030171312A1
; GENERAL INFORMATION:
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Matches 125; Conservative
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CORGANISM: Homo sapiens
US-09-845-416-33
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-845-416-26
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121 GCCAA 125
                                121 GCCAA 125
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LENGTH: 955
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Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICANT: XAPO

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT APPLICATION NUMBER: 60/200,777

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SSOTHARE: Patentin Ver. 2.1

SSOTHARE: Patentin Ver. 2.1

LENGTH: 955
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                                                                                                                                                                                                                                                                                                                                                          FEATURE:

COTHER INFORMATION: synthetic enzyme attachment site sequence
US-10-023-208-58
                        Sequence 58, Application US/10023208

Dublication No. US20030124537A1

GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Win
APPLICANT: Li, Win
APPLICANT: Li, Win
APPLICANT: Li, Win
CURRENT APPLICANTON: PROCARYOTIC LIBRARIES AND USES
FILE REPERENCE: A-70174-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/256,163
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.1
SEQ ID NO SE
                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 125; Conservative
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CORGANISM: Homo sapiens
US-09-845-416-26
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US-09-845-416-26
                  JS-10-023-208-58
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TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TILE REPERENCE: DELIAZ.
CURRENT APPLICATION NUMBER: US/09/845,416
CURRENT PILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,777
PROR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PALENTIN Ver. 2.1
LENGTH: 987
US-05-845-416-26/C
US-05-845-416-26/C
US-05-845-416-26/C
Sequence 26, Application US/09845416
PUBLICATION NO. US2030171312A1
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE PEPERRORCE: DB1142
CURRENT APPLICATION NUMBER: 60/200,777
PRIOR APPLICATION NUMBER: 60/200,777
PRIOR APPLICATION NUMBER: 60/200,777
NUMBER OF SEQ ID NGS: 36
NUMBER OF SEQ ID NGS: 36
SOFTWARE: PatentIn Ver. 2.1
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Search completed: April 1, 2004, 18:36:00 Job time : 189.426 secs
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ORGANISM: Homo sapiens
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| Publication No. US20030171312A1 |
| GENERAL INPORMATION: |
| APPLICANT: XIAO, XIAO |
| TITLE OF INVENTION: DNA SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE |
| TITLE OF INVENTION: THRREOF |
| TITLE OF TABLICATION NUMBER: US/09/845,416 |
| CURRENT APPLICATION NUMBER: 60/200,777 |
| PRIOR APPLICATION NUMBER: 60/200,777 |
| PRIOR PTLING DATE: 2001-04-28 |
| NUMBER OF SEQ ID NOS: 36 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 32 |
| LENGTH: 4414
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| Sequence 313 Application US/09845416
| Sequence 313 Application US/09845416
| Publication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICAMY KIADA XIADA
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILLE REFRENCE: DE1142
| CURRENT APPLICATION NUMBER: US/09/845,416
| CURRENT FILING DATE: 2001-04-30
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: PATENTIN VET. 2.1
| SEQ ID NO 33
| LENGTH: 987
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CRGANISM: Homo sapiens
US-09-845-416-32
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CORGANISM: Homo sapiens
US-09-845-416-33
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US-09-845-416-32/c
; Sequence 32, Application US/09845416
; Publication No. US2003171312A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: UNMBER: US/09/845,416
; CURRENT FILING DATE: 2001-04-30
; PRIOR PILICATION NUMBER: 60/200,777
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 32
; LENGTH: 4414
1 TTGGCCACTCCCTCTTGGGCGCTCGCTCGCTCAAAGGCCGGGCGACAAAGGTCGCC 60
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Best Local Similarity 100.0%; Pred. No. 6.3e-26;
Matches 125; Conservative 0; Mismatches 0; Indels 0;
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Title: Perfect score:

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Sequence 1, Application US/07789917A

Patent No. 552479

GENERAL INFORMATION:
APPLICANT: STIVASETAVA, Arun
TITLE OF INVENTION: SAFE VECTOR FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy Presser
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
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ZIP: USA
ZIP: USA
ZIP: USA
ZIP: USA
COMPUTER READABLE FORM:
MEDIUM TYEE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release q.0, Version q.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,917A
FILING DATE: 19911118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCNULLY, William E.
REGISTRATION NUMBER: 22,606
REFERENCE/DOCKET NUMBER: 8361
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECAME. (516) 742-4366
TELECAME. (
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US-09-296-141-5
US-09-276-655-4
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Sequence 9,
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1: /cgn2_6/ptodate/2/ina/5A_COMB.seq:*
 /cgn2_6/ptodate/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodate/2/ina/6A_COMB.seq:*
 /cgn2_6/ptodate/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodate/2/ina/PCTUS_COMB.seq:*
                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-07-982-193-1
US-08-471-914-1
US-08-276-625-7
US-08-254-358-1
US-08-25-178-1
US-08-29-114-4
US-09-29-114-4
US-09-29-141-4
US-09-299-141-4
US-09-299-141-8
US-09-299-141-8
US-08-893-327-15
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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APPLICANT: LATTA,
APPLICANT: DENEFLE, Patrice
APPLICANT: UGNE, Emmanuelle
APPLICANT: VIGNE, Emmanuelle
APPLICANT: VIGNE, EMMANUELE
APPLICANT: PERRICADDE, MIChel
TITLE OF INVENTION: INTEGRATIVE RECOMBINANT ADENOVIRUSES,
TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
NUMBER OF SEQUENCES: 13
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcole Rd. 3C43
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Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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LOCATION: 1...145
OTHER INFORMATION: /note= "Minimal ITR Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:

CLASSIFICATION DATA:
PROOF APPLICATION DATA:
PROOF APPLICATION DATA:
PROOF APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
PROOF APPLICATION DATA:
APPLICATION NUMBER: WO PUT/FR95/00233
FILING DATE: 28-FEB-1995
ATTOMREY/AGRET INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REPRERENCE/DOCKET NUMBER: 38,619
REPRERENCE/DOCKET NUMBER: 38,619
RELEPRANTION INFORMATION:
TELEPRANTION INFORMATION:
TELEPRANTION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
TENDTH: 145 base pairs
                                                                   121 GCCAACTCCATCACTAGGGGTTCCT 145
                                                                                                         121 GCCAACTCCATCACTAGGGGTTCCT 145
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US-08-702-573-4
; Sequence 4, Application US/08702573
; Patent No. 6033865
; GENERAL INFORMATION:
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STRANDEDNESS: double
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MOLECULE TYPE:
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COMPUTER: IBM PC_compatible
OPERATURG SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,193
FILING DATE: 19921125
CLASSIFICATION: WINSER: 22 666
REFERENTION: William E.
REGISTRATION NUMBER: 22 666
REFERENCE/DOCKET NUMBER: 8361
TELECOMMUNICATION INFORMATION:
TELEFRACE (516) 742-4366
TELEFAX: (516) 742-
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APPLICANT: Samulski, R. J.
APPLICANT: Xiao, X.
APPLICANT: Xiao, X.
TITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                    US-07-982-193-1
) Sequence 1, Application US/07982193
) Sequence 2, Application US/07982193
) Patent No. 6261834
) GENERAL INFORMATION:
APPLICANT: SITVASIEVA, Arun
TITLE OF INVENTION: SAFE VECTOR FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE S. 2
) GORESPONDENCE ADDRESS:

STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-07-982-193-1
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity
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US-07-989-841A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 145; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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Patent No. 6657152
GENERAL INFORMATION:
APPLICANT: Samulski, R.
APPLICANT: Xiao, X.
TITLE OF INVENTION: RECOMBINANT VIRAL VECTOR SYSTEM
FILE REPERSNCE: 6636-027
CURRENT RILING DATE: 1995-06-06
BARLIER PLING DATE: 1995-06-15
CURRENT PLING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 165
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FILING DATE: May 15, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 6636-0
TELECOMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEPA: (212) 869-8864/9741
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-440-738A-1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-471-914-1
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APPLICANT: Samulski, R. J.
APPLICANT: Xiao, X.
APPLICANT: Xiao, X.
TITLE OF INTENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
CUTY: New York
CUTY: New York
COMPUTER: 1150 Avenue of the Americas
COMPUTER: 1150 Avenue of the Americas
COMPUTER: 1150 Avenue of the Americas
STRIE: 1005-2711
COMPUTER: 1180 PC Compatible
COMPATICATION NUMBER: US/08/440,738A
                                                                                                                             STATE: New York

CUNTRY: U. S.A.

ZIP: Nose York

CONTRY: U. S.A.

ZIP: 10036-271

ZIP: 10036-271

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: LBM FC Compatible

COMPUTER: LBM FC COMPATION:

NAME: COMPUTER: LBM FC COMPATION:

NAME: COMPUTER: LBM FC COMPATION:

TELEFAX: (212) 869-8664/9741

TELEFAX: (212) 869-8664/9741

TELEFAX: (212) 869-8664/9741

TELEFAX: CALA PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LBMGTH: LSE DASS PAISE

TELEFAX: CALA PENNIE

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4.3e-31;
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Best Local Similarity 100.0%; Pred. No. 4
Matches 145; Conservative 0; Mismatche
                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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MOLECULE TYPE: DNA (genomic)
          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-440-738A-1
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US-US-47-391-1

SEQUENCE 1, Application US/08475391

Patent No. 5786311

GENERAL INPOMATION:

TITLE OF INVENTION: Adeno-Associated Virus Materials and

TITLE OF INVENTION: Methods

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: ACREASE:

ADDEESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 6066

COMPUTER READABLE FORM:

MEDIUM TYPE: FLORPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PCTOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CLASSIFICATION NUMBER: US/08/475,391

FILING DATE: 07-UNN-1995

PRIOR APPLICATION DATA:

PRILICATION NUMBER: US/254,358

PRIOR APPLICATION DATA:

PRILICATION NUMBER: US/254,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 145; DB 1; Length 4680; Best Local Similarity 100.0%; Pred. No. 5.8e-31; Matches 145; Conservative 0; Mismatches 0; Indels 0
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NAME: No. 5786211and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELECOMMUNICATION INFORMATION:
TELEBRIONE: (312) 474-6300
TELEBRX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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TELEFAX: (312) 474-6448
TELEFX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: lir
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US-08-475-391-1
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; OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. 6436392 5,478,745
US-09-276-625-7
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Jeduence 1, Application Methods

Jeduence
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.007031
CURRENT RILING DATE: 1999-03-25
CURRENT FILING DATE: 1999-03-25
PRIOR PAPLICATION NUMBER: US 60/086,166
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 165
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141 GCCAACTCCATCACTAGGGGTTCCT 165
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658785and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
                                                                                                                                                                                                                                           US-09-276-625-7; Sequence 7, Application US/09276625; Patent No. 6436392; ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-254-358-1
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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; Bequence 1, Application US/08709609
; Patent No. 585875
; GENERAL INFORMATION:
    APPLICANT: Obnson, Philip R.
    TITLE OF INVENTION: Methods
    TITLE OF INVENTION: Methods
    NUMBER OF SEQUENCES: 3
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
    CITY: Chicago
    STATE: Illings
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4680;
                             100.0%; Score 145; DB 1; Length 4680; 100.0%; Pred. No. 5.8e-31; ive 0; Mismatches 0; Indels 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
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100.0%; Score 145; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 145; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                       121 GCCAACTCCATCACTAGGGGTTCCT 145
                                                                                                                                                                                                                                             121 GCCAACTCCATCACTAGGGGTTCCT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                           Query Match
Best Local Similarity 100.
Matches 145; Conservative
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US-08-475-391-1
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-299-141-4
Sequence 4, Application US/09299141
Sequence 4, Application US/09299141
Patent NO. 6461606
GENERAL INFORMATION:
APPLICANT: FLOTTE, TERENCE R.
APPLICANT: BYENE, B
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGERT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFREENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TORRANTION:
TELECOMMUNICATION TORRANTION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRACTH: 4680 base pairs
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100.0%; Score 145; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 145; Conservative 0; Mismatches 0;
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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121 GCCAACTCCATCACTAGGGGTTCCT 145
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                     Length 5932;
                                                                                                                                                                                                                                                         ; FEATURE:
. OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4
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US-09-199-141-4/C
is-09-299-141-4/C
is-09-299-141-4/C
sequence 4, Application US/09299141
Patent No. 6461606
GENERAL INFORMATION:
APPLICANT: FLOTTE: TERRNCE R.
APPLICANT: FLOTTE: TERRNCE R.
APPLICANT: MORGAN, MICHAEL
TITLE OP INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REPERENCE: 4300-011800
CURRENT APPLICATION NUMBER: 05/09/299,141
CURRENT FILING DATE: 1999-04-23
SAPTHARE PILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO S: 532
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, OTHER INFORMATION: Description of Artificial Sequence:p43C-ATUS-09-299-141-4
                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 145; DB 4; Length 59
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 4300.011800
CURRENT APPLICATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/083,025
BARLIER FILING DATE: 1998-04-24
NUMBER OF SEG ID NOS: 13
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                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                              SEQ ID NO 4
LENGTH: 5932
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Sequence 8, Application US/0929141

Sequence 8, Application US/0929141

Sequence 8, Application US/0929141

Patent No. 6461606

GENERAL INPORMATION:
APPLICANT: SONG, SIRONG

APPLICANT: BYRNE, BARKY J.
APPLICANT: BYRNE, BARKY J.
APPLICANT: MORGAN, MICHAEL

TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REFERENCE: 4300.01180

CURRENT FILING DATE: 1999-04-23

CURRENT FILING DATE: 1998-04-24

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 6142
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Sequence 8, Application US/09299141

Sequence 8, Application US/09299141

Patent No. 645106

APPLICANT: FLOTTE, TERENCE R.

APPLICANT: SONG, SIMONG

APPLICANT: BARRY J.

TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

FILE REFERENCE: 1300.011800

CURRENT FILING DATE: 1999-04-23

EARLIER APPLICATION NUMBER: 60/083,025

EARLIER APPLICATION NUMBER: 60/083,025

EARLIER PILING DATE: 1999-04-24

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 6142
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100.0%; Score 145; DB 4; Length 61
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 145; Conservative 0; Mismatches 0; Indels
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Job time : 65.7593 secs
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April 1, 2004, 12:58:58; Search time 243.815 Seconds (without alignments) 2526.461 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                             3373863 seqs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Maximum DB seg length: 2000000000
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Perfect score:
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	Description	Aaq41448	Aat 03385	Aax34295	Abs69884	Acc58491	Ac£35876	Abx93568	Aaq66769	Aat 49462	Aad03535	Abs69886	Abv77279	Aad44621	Aad37254	Aad37254	7261	Aad37261	Aad37260	Aad37260	Aad37259	Aad37259	Aad37258	Aad37258
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SUM		AAQ4144	AAT0338	AAX3429	ABS69884	ACC58491	ACF3587	ABX93568	AAQ66769	AAT49462	AAD03535	ABS69886	ABV77279	AAD44621	AAD37254	AAD37254	AAD3726	AAD3726	AAD37260	AAD37260	AAD37259	4AD37259	AAD37258	AAD372
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ALIGNMENTS

RESULT	RESULT 1	
{ax	AAQ41448 standard;	ard; DNA; 145 BP.
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	AAQ41448;	
설립	25-MAR-2003 (revised)
- X		(rirst entry)
图	AAV2 inverted	terminal repeat.
X ₹	Adeno-associated virus	gration; vecto
3 2	cell-specific; sickle cell an	cell-specific; gene therapy; haemoglobinopathies; thalassemia; diabetes; sickle cell anaemia; cancer; parvovirus; B19; ss.
X 8	Adeno-associated virus	ed virus 2.
X E	Key	Location/Qualifiers
FFFF	repeat_region	 1.125 /*tag= a /noerted terminal repeat forming palindromic hairpin"
FFFX	misc_feature	4283 /*tag= b /note= "Flip orientation"
(A)	WO9309239-A1.	
(문)	13-MAY-1993.	
ζ£4>	06-NOV-1992;	92WO-US009769.
5 E S	08-NOV-1991;	91US-00789917.
{ E }	(RESE) RESEAR	RESEARCH CORP TECHNOLOGIES INC.
SES	Srivastava A;	
1 1 1 1 1 1 1	WPI; 1993-167704/20	04/20.
1	Adeno-associated virus-2 of haemoglobinopathies an	Adeno-associated virus-2 basal vectors - for gene therapy and treatment of haemoglobinopathies and cancer etc has cassette contg. a promoter
I E A	of the adeno-a	dayiesion, beereen rirus 2.
5 E	Disclosure, Fi	Fig 1; 68pp; English.

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The sequence is one of two inverted terminal repeat sequences, one from parvovirus B19 and the other from adeno-associated virus 2 (AVV), used in construction of an expression vector for site specific integration and cell specific gene expression. The vector comprises at least one cassette contg. a promoter capable of effecting cell-specific expression, operably linked to a hetero-logous gene, and the cassette residing between the inverted terminal repeats. The vector is safe for use in gene therapy, partic. In treatment of haemoglobinopathies and a variety of diseases, e.g. thalassemia, diabetes, sickle cell anaemia, and cancer. See also AAQ41449. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant, non-pathogenic adenovirus which are able to integrate stably into a host genome are claimed. The viruses pref. contain at least one inverted terminal repeat (TTR) sequence and in particular two TTRs flank a heterologous DNA insert. The present sequence is that of the strict TTR from adeno associated virus AAV-2 (i.e. the ITR sequence without any deletions or additions). In the construct pITRFL, the beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                         61 caacecccesecririecccesececcrcaereaeceaeceaececececaeaeaeaece 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inverted terminal repeat; ITR; adenovirus; adeno-associated virus; AAV-2; replication defective; integration; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                     1 TIGGCCACTCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant defective adenovirus contg. integratable expression cassette - for use in gene therapy to express protein, antigen or anti:sense nucleic acid, also for prodn. of recombinant adeno-associated viruses.
                                                                                                                                                                                                                                                                                                                                                 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 145; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.1e-30;
Matches 145; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strict inverted terminal repeat from AAV-2, used in pITRFL
                                                                                                                                                                                                                                Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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(first entry)
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18-APR-1996
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marker gene is flanked by two strict AAV-2 ITRs, The defective viruses are useful for stably introducing large fragments of heterologous DNA making them suitable for gene therapy. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTGGCCACTCCCTCTCTGCGCTCGCTCGCTCAGGGCCGAGCCGGGCGACCAAGGTCGCC
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promoter; rep; cap; inverted terminal repeat; ITR; erythroid cell
integration; gene expression; bone marrow; peripheral blood cell;
endothelial cell; myocardial cell; ss.
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0
                                                                                                                                                                                                                                             Length 145;
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                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                          49 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         100.0%; Score 145; DB 2;
100.0%; Pred. No. 8.1e-30;
ive 0; Mismatches 0;
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                                                                                                                                                                              Sequence 145 BP; 21 A; 52 C;
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Best Local Similarity 100.
Matches 145, Conservative
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AAX34295

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Length

DB 2;

100.0%; Score 145;

Query Match

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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (NS) having 5' and 3' end, left and right inverted terminal repeats of adenovirus flanking NS, adenovirus packaging sequence linked to inverted terminal repeat, and adeno-associated virus terminal repeat linked to 3' end of NS, into cell expressing adenovirus early gene lacking from vector; and culturing cell to produce another vector. The method is useful for generating vectors, especially mAd vectors The method is useful in transferring nucleotide sequences of interest into a cell, for gene transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo. The nucleotide sequences are useful for treating diseases associated with the control of the nucleotide degree are useful for treating diseases associated with the control of the nucleotide degree of interest into diseases associated with the denosting diseases as the nucleotide degree of the associated with adenosting deaminase the control of the nucleotide degree of the nuc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector; adenovirus; adeno-associated; adenosine deaminase gene; recepte adenoine deaminase deficiency; severe combined immune deficiency; PAH beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; hypoxanthine-guanine phosphoribosyltransferase; lesch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylkeconuria; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antilipaemic; noctropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds
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haemoglobin gene associated with beta-thalassaemia and sickle cell
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                                                                         Indels
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                           Pred. No. 8.1e-30;
Mismatches 0;
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100.08; FL
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Matches 145; Conservative
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disease, receptor for low density lipoprotein gene associated with familial hypercholesterolaemia, hypoxanthine-guanine phosphorizansferase associated with leach-Whan syndrome, phosphorizansferase associated with leach-Whan syndrome, dystrophin gene associated with muscular dystrophy, and human cystic fibrosis transmembrane conductance regulator gene associated with cystic fibrosis. The present nucleic acid sequence represents a human adenossociated virus 2 (AAV2) terminal repeat sequence that was used in the methods of the invention
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                                                                                                                                                                                                                                                                                                                       Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;
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100.0%; Pred. No. 8.1e-30;
iive 0; Mismatches 0;
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13-AUG-2002; 2002US-00216870.
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ACC58491 standard; DNA; 145
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Matches 145; Conservative
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The invention relates to a recombinant adenovirus comprising an adenovirus that encodes one or more AAV REP78/68 polypeptides that are inducibly expressed. A complete virus-mediated system for recombinant AAV production is provided which comprises: (a) a first recombinant adenovirus encoding one or more AAV REP78/68 polypeptides and one or more viral capsid polypeptides; (b) a second recombinant adenovirus comprising a gene of interest and AAV inverted terminal repeats that flank the gene of interest; (c) viral heiper functions; and (d) a host cell comprising the first recombinant adenovirus, the second recombinant adenovirus, and the viral heiper functions. The recombinant AAV is useful as a vector for gene therapy. The present sequence represents an AAV-2 left inverted terminal repeat (ITR) sequence
ITR and coding sequences for AAV VP1, VP2 and VP3 capsid proteins, for AAV non-structural replication (Rep) proteins Rep52 or Rep40, and for AAV Rep78 or Rep68. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
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                                                                                                       Sequence 145 BP; 23 A; 49 C; 52 G; 21 T; 0 U; 0 Other;
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100.0%; Score 145; DB 7;
Best Local Similarity 100.0%; Pred. No. 8.1e-30;
Matches 145; Conservative 0; Mismatches 0;
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Sequence 145 BP; 21 A; 52 C; 49 G; 23 T; 0 U; 0 Other;

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viral regulatory element.
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sequence"
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/bound_moiety= "Nucleotides 62-54 of the present
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/label= Rep recognition sequence
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100.0%; Score 145; DB 8;
100.0%; Pred. No. 8.1e-30;
ive 0; Mismatches 0;
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54. .62
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                                                                                                                                                                                                                                                                                                                    The invention relates to identifying molecules that interact with an adeno-associated viral regulatory element (e.g. a Rep recognition sequence, RRS) comprising contacting at least one molecule with a nucleic sequence, RRS) comprising on adeno-associated viral regulatory element, and identifying whether at least one molecule is bound to the viral requiatory elements. Also included is a kit for analysing the interaction between molecules and an adeno-associated viral regulatory element. The method is useful for identifying molecules e.g. at least one cellular protein, synthetic protein or exogenous protein proteins that are derived from a cDNA library or cellular lysate), or peptide, antibody, nucleic acid, lipid, carbohydrate and/or organic or inorganic compound that interacts with an adeno-associated virus (AAV) and facilitates the application of adeno-associated virus (AAV) and facilitates the application of adeno-associated virus-based vector system, therefore ITR-binding proteins and other molecules provide new insights into the AAV life cycle, including the requisition of gaseciated virus-based vector system, therefore ITR-binding proteins and other molecules provide new insights into the AAV life cycle, including the requisition of gaseciated virus-based vector system, therefore ITR-binding proteins and improvements for its application in therapy. The present sequence is an AAV-2 ITR containing an RRS used in the method of the invention
                                                                                                                                                                                                        contacting an adeno-associated viral regulatory interacting molecule with a nucleic acid comprising a adeno-associated viral regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of cellular regulations of adeno-associated virus involves contacting an adeno-associated viral regulatory interacting molecule with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 145; DB 7; Length 146; 100.0%; Pred. No. 8.1e-30; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAACTCCATCACTAGGGGTTCCT 145
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                                                                                                                                                                                                                                                                              Disclosure, Fig 1; 16pp, English.
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                                                                           Cathomen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 145; Conservative
(WEIT/) WEITZMAN M D. (CATH/) CATHOMEN A J.
                                                                                                                            WPI; 2003-328607/31
                                                                           Weitzman MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9413788-A1
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20-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .165
/*tag= m
/label= Double-D
a secent Display sequence, resulting from addition of
a secend D repeat to the AAV ITR, has not been identified
in any naturally occurring virus"
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/standard name= "ITR"
/note= "This naturally occurring 145 bp ITR is located at
both ends of the AAV genome"
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                                                                                                                                                                                                                                                                                                  Adenovirus associated viral inverted terminal repeat - for use in recombinant viral vector system for treatment of genetic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 145; DB 2; Length 165; 100.0%; Pred. No. 8.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25; 44pp; English
93WO-US011728.
                                                          92US-00989841
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                                                                                                                                                                                Samulski RJ, Xiao X;
                                                                                                                                                                                                                                              WPI; 1994-217868/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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(ITR) located at each end of its genome. In addition to being able to the see pair with each other, the ITRs can also individually fold back on themselves through the base pairing of A, A', B, B' and C, C' sequences to form a T-shaped structure for DNA replication (see features table). It has been found that viral mutants with deleted D sequences are unable to replicate their DNA. Addition of a second D repeat (D') to the naturally occurring ITR resulted in a sequence, designated double-D, which was sufficient to carry out the functions normally required of two wild-type ITRs during a lytic AAV viral infection, i.e. it is capable of directing replication and assembly into AAV, and/or the integration into the host genome, of recombinant DNA containing the nucleic acid molecule. Vectors and viral particles containing the double-D sequence are useful in gene therapy. Replication and integration into the host genome is completely effected through the double-D sequences, ensuring that the heterologous
                                                                                                                                                                                                           Length 165;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                    Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
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                                                                                                                                                                                                         Query Match
100.0%; Score 145; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inverted terminal repeat double DD DNA sequence.
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                                                                                                                                                               gene sequences remain intact
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(ENGE/) ENGELHARDT J F.
(DONG/) DONGSHENG D.
(ZIYI/) ZIYING Y.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAD03535 standard; DNA; 165
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/labol= A' repeat
/note= "forms the stem of a T-shaped structure when base
paired with repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a T-shaped structure when base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Double-D sequence directs adeno-associated virus integration into host genome - used in gene therapy, maintains full length coding sequence of therapeutic gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The adeno associated virus (AAV) has a 145 bp inverted terminal repeat
                                                                                                                                                                                                                                                                                                                                   /*tag= k
/note= "Part of T-shaped structure, formed by base
pairing between the B' and B repeats"
85. .92
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//rag= j
/note= "Part of T-shaped structure, formed by base
pairing between the C' and C repeats"
63. /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Additional D' sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_type= INVERTED
/label= A repeat
/note= "Forms the stem
paired with A' repeat"
                                                                                                                                                                                                                                                                                               /rpt_type= INVERTED
/label= C_repeat
84. 104
                        /rpt_type= INVERTED
/label= D_repeat
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label= C'_repeat
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'label= B_repeat
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/label= D'
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                                                   misc_structure
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                                                                                                                                                                Recombinant adeno-associated virus; rAAV; circular intermediate; ITR; inverted terminal repeat; haemostatic; antisickling; neuroprotective; antiansemic; noctropic; blood disorder; sickle cell anaemia; thalassaemia; neurological disorder; haemophilia; Alzheimer's disease; muscle disorder; Parkinson's disease; gene delivery; erythropoietin; el CFTR; cystic fibrosis transmembrane conductance receptor; tyrosine hydroxylase; gluccerebrosidase gene; Gaucher's disease; gene therapy; bouble DD; ds.
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Gaps
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01-AUG-2002.

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The patent discloses a composition comprising at least two recombinant adeno-associated viruses (rAAVs). Each rAAV contains a recombinant DNA molecule comprising three DNA segments linked together. The first and the third DNA segments comprises 5' and 3' inverted terminal repeats (ITRS) respectively from the circular intermediate of AAV. The second DNA segment in each virus is different and does not comprise AAV sequence. To propagate such as the cystic fibrosis transmembrane conductance polypeptide such as the cystic fibrosis transmembrane conductance receptor gene (PRTR), the erythropoietin (epo) gene, the tyrosine receptor gene (PRTR), the erythropoietin (epo) gene, the tyrosine receptor gene (PRTR) and persistence of the vector in the host cell. Outpositions comprising rAAV sequences are useful for transferring recombinant DNAs to a host cell and express a polypeptide in a host cell are treatment or prophylaxis of blood disporders (e.g. shoth cell anaemia, than assemmia, hammorphilia), neurological disorders, such as Alzheimer's disease, Parkinson's disease, muscle disorders involving skeletal, cardiac or smooth muscle. AAV vector is used as a dalivery vehicle for gene therapy. The present sequence is used as a dalivery vehicle for as "double sequence". This sequence is the ITR DD DNA sequence referred to as "double sequence". This sequence is the present invention
Composition for transferring recombinant DNAs and to express a polypeptide in a host cell, comprises two recombinant adeno-associated viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 165 BP; 27 A; 56 C; 56 G; 26 T; 0 U; 0 Other;
                                                                                                                                    Disclosure, Page 139; 144pp; English.
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Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0; Indels C GCCAACTCCATCACTAGGGGTTCCT 145 141 GCCAACTCCATCACTAGGGGTTCCT 165 19 87 21 ద ð g ò ò g

ABS69886 standard; DNA; 165 BP. 21-NOV-2002 (first entry) ABS69886

Human adeno-associated virus 2 terminal repeat DD sequence.

Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor; adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; hypoxanthine-guanine phosphoribosyltransferase; lasch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylketomuria; dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; antianaemic; antilipaemic; noorropic; cytostatic; cegulator gene; antilipaemic; noorropic; cytostatic; dermatological; human adeno-associated virus 2; AAV2; terminal repeat; ds.

US2002102731-A1

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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having uncleotide sequence (NS) having 5' and, left and right inverted terminal repeats of adenovirus packaging sequence linked to inverted terminal repeats of terminal repeats of adenovirus packaging sequence linked to inverted terminal repeat linked to 3' end of NS, into cell expressing adenovirus early gene lacking from vector of and culturing cell to produce another vector. The method is useful for generating vectors, especially mAd vectors. The method is useful in transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase (CT the mucleotide sequences are useful for treating diseases associated with asemplobin gene associated with beta-thalassemia and sickle cell to adenosibe deaminase gene associated with its ever combined immune deficiency, beta-chain of the managiopin gene associated with its ever combined immune deficiency, beta-chain of the coptor for low density lipoprotein gene associated with heach. Nyhan syndrome, the phosphoribosyltransferase associated with its everted with mescular dystrophy, and human cystic fibrosis transmembrane conductance regulator gene associated with expresents a human adenotic associated virus 2 (AAVVZ) terminal repeat sequence that was used in the
                                                                                                                                                                                                                                                                                                                 adenovirus inverted terminal repeats and packāging sequence, and adeno-
associated virus terminal repeat, into cell, and culturing cell.
                                                                                                                                                                                                                                                                                              Producing vector, by introducing vector having nucleotide sequence,
                                                                                                                                                                                               Gnatenko DV;
                                                                                                                                               (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                               Sandalon Z,
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 8; 191pp; English.
                                                                                                  02-OCT-2000; 2000US-0237747P.
                                               12-FEB-2001; 2001US-0078237B.
                                                                                                                                                                                                                                                 WPI; 2002-690619/74.
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0; Gaps 100.0%; Score 145; DB 6; Length 165; 100.0%; Pred. No. 8.2e-30; ative 0; Mismatches 0; Indels Seguence 165 BP; 24 A; 59 C; 53 G; 29 T; 0 U; 0 Other; Query Match
Best Local Similarity 100.0
Matches 145; Conservative

methods of the invention

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1 INGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC

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121 GCCAACTCCATCACTAGGGGTTCCT 145 141 GCCAACTCCATCACTAGGGGTTCCT 165 셤 ઠ g ò g

Nucleotide sequence of pTRT, a circular adeno-associated virus. ABV77279 standard; DNA; 165 28-MAR-2003 (first entry) ABV77279;

RESULT 12

Circular adeno-associated virus; cAAV; replication; hairpin; gene therapy; pTRT; ss.

14-DEC-2001; 2001WO-US049058

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31-MAY-2001; 2001US-0294797P.
                                                                                                     31-MAY-2002; 2002WO-US017324
                                                                                                                                                                                                                              Kaplitt MG, Moussatov S;
                                                                                                                                                                                      (UYRQ ) UNIV ROCKEFELLER
Adeno associated virus
                                                                                                                                                                                                                                                                WPI; 2003-103706/09
                                 WO200297056-A2
                                                                     05-DEC-2002
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The specification describes a nucleotide sequence capable of directing circular adeno-associated virus (CAAV) replication. This nucleotide sequence comprises a loop sequence (TGGCAAA) finhwed on the 5' and 3' sides by complementary sequences, where a hairpin structure is formed between the complementary sequences. The CAAVs are useful in gene therapy, e.g. to treat an acute medical condition a nucleic acid encoding a therapputic protein is inserted into the cAAV. The present sequence represents pTRT, a cAAV that contains a wild-type dircularization point (the TRT domain), consisting of a single ITR flanked by two D-sequences Production of defective viral vectors for gene therapy that are completely free of helper viral vectors and helper viruses. Example 4; Page 53; 69pp; English

Sequence 165 BP; 26 A; 56 C; 56 G; 27 T; 0 U; 0 Other;

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                                                                               145 TTGGCCACTCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGGGAAAGTCGCC
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Query Match
100.0%; Score 145; DB 7;
Best Local Similarity 100.0%; Pred. No. 8.2e-30;
Matches 145; Conservative 0; Mismatches 0;
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Prokaryotic library; candidate protein; nucleic acid modification; NAM; enzyme attachment sequence; EAS; clinical pharmacology; chemical sensor; enzymology; cosmetic research; toxic; environmental safety assessment; nutrient blology; enzyme attachment site; EAS; ds.
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                                                                                                                                              AAD44621 standard; DNA; 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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RESULT 13
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LID AAD
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WO200266653-A2

29-AUG-2002

The invention relates to methods and compositions for the construction of prokaryotic libraries expressing candidate proteins and the use of these libraries to identify candidate proteins and the nucleic acids encoding them. The invention provides a library of prokaryotic pET-24a vectors comprising a fusion nucleic acid consisting of anucleic acid encoding a nucleic acid modification (NAM) enzyme or a candidate protein, or a cuncleic acid having a T7 promoter operably linked to the NAM enzyme or the candidate protein, and an enzyme attachment sequence (EAS) recognised by the NAM enzyme. The library is used for identifying candidate proteins and nucleic acids encoding these proteins, or in screening for NAM enzymes with decreased toxicity for the host cells, or in identifying novel or improved EASs, which may be used for understanding cellular processes or improved EASs, which may be used for understanding cellular processes or any subsequent therapeutic or toxic activities. The nucleic acid/protein (NAP) conjugates are useful in diagnostic assays and in research capturicular chemicals, environmental safety assessment, chemicals, environmental safety assessment, chemicals, environmental safety assessment, chemical sensor, nutrient biology, cosmetic research or enzymelogy. These may also be used in in vitro screening techniques and in assays with target molecules. The information of the interview. 42 TIGGCCACTCCCTCTCTGCGCGCCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 101 New library of prokaryotic pET-24a expression vectors, host cells or nucleic acid/protein conjugates, useful for screening candidate proteins and their nucleic acids or modification enzymes for pharmacogenetic 1 TIGGCCACTCCCTCTGCGCGCTCGCTCACTGAGGCCGGGCGAAAGGTCGCC Gaps . 0 Length 207; 0; Indels Sequence 207 BP; 36 A; 68 C; 68 G; 35 T; 0 U; 0 Other; / Match
Local Similarity 100.0%; Pred. No. 8.3e-30; Pes 145; Conservative 0; Mismatches 0; 121 GCCAACTCCATCACTAGGGGTTCCT 145 162 GCCAACTCCATCACTAGGGGTTCCT 186 Disclosure; Fig 50B; 127pp; English 14-DEC-2000; 2000US-0256163P. WPI; 2002-667068/71. (XENC-) XENCOR INC Liu Y; 102 Query Match Best Loca Matches Li M, RESULT 14 В ò $\stackrel{>}{\circ}$

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds. Adeno-associated virus (AAV) vector plasmid #1. BP. AAD37254 standard; DNA; 955 (first entry) 21-AUG-2002 AAD37254;

Homo sapiens Unidentified

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The present invention relates to an isolated nuclectide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, Hi and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (bMD) and Becker muscular dystrophy (bMD) and Becker muscular dystrophy (bMD) and sector and a small polyA signal sequence
                                                                                                                                                                                                                                                                                                                                                   New dystrophin minigene for treating Duchenne or Becker muscular
dystrophy comprises an N-terminal domain or modified N-terminal domain,
rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 57; 71pp; English.
                                                                                                                                27-APR-2001; 2001WO-US013677.
                                                                                                                                                                           28-APR-2000; 2000US-0200777P
                                                                                                                                                                                                                                                                                                         WPI; 2002-049342/06.
                                                                                                                                                                                                                     (XIAO/) XIAO X.
                                          WO200183695-A2
                                                                                      08-NOV-2001.
Chimeric.
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                    Adeno-associated virus (AAV) vector plasmid #1.
                       AAD37254 standard; DNA; 955
                                                                (first entry)
                                                                 21-AUG-2002
                                            AAD37254;
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Homo sapiens. Unidentified. Chimeric.

WO200183695-A2

27-APR-2001; 2001WO-US013677.

28-APR-2000; 2000US-0200777P

(XIAO/) XIAO X.

Kiao X;

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin

Example 1; Page 57; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence

Sequence 955 BP; 177 A; 307 C; 296 G; 175 T; 0 U; 0 Other;

896 9 955 TTGGCCACTCCCTCTCTCTGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 1 TIGGCCACICCCICICIGCGCGCTCGCTCGCTCACIGAGGCCGGGCGACCAAAGGICGCC Gaps . 100.0%; Score 145; DB 6; Length 955; 100.0%; Pred. No. 9.1e-30; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 145, Conservative Local Similarity Query Match 셤 ò

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120 61 CGACGCCCCGGGCCGGCCGCCTCAGTGAGCGAGCGAGCGCCAGAGAGGGAGTG ð 엄

121 GCCAACTCCATCACTAGGGGTTCCT 145 835 GCCAACTCCATCACTAGGGGTTCCT 811 ઠ

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12	145	100.0		9	AX286292	AX286292 Sequence
13	145	100.0		9	AX753252	AX753252 Sequence
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53	145	100.0		9	AR235459	AR235459 Sequence
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m	145	100.0		9	AR235462	AR235462 Sequence
c 32	145	100.0		9	AR235462	AR235462 Sequence
m	145	100.0		9	AR235463	AR235463 Sequence
c 34	145	100.0		9	AR235463	AR235463 Sequence
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COMMENT

ORIGIN

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/organism="Adeno-associated virus 2H"

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[2]), from KB or HeLa cells.

[2]), from KB or HeLa cells.

[2]) from KB or HeLa cells.

Both [1] and [2] present the opposite strand from the one presented here. The focus of both papers is the method of replication of the virus. [1] notes that the initial tt is present only 30% of the time; it is shortened to t in 50% of the population and missing altogether in 15% of the population. There is further sequence heterogeneity which can be explained by assuming that the terminal 125 bases, which form an imperfect palindrome, are replaced by their inverted complement during replication. [2] found that deletion of the 9 terminal bases on the right and the 113 terminal bases on the left of AAV 2 genome did not stop DNA replication. Further deletion of an Il-base symmetrical sequence (bases 89 to 99) in the right terminal repetition inhibits DNA replication. Substitution of either an 8-base (cagatctg) or 12-base (cagatctgc) symmetrical sequence unrelated to the original 11-base sequence restores DNA replication. All of this can be explained by assuming that the 125 base palindrome mentioned above form at t-shaped secondary structure which provides a primer for DNA polymerase during replication.

Location/Qualifiers
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Adeno-associated virus 2H
Yuruses; seDNA viruses; Parvovirinae; Dependovirus.
(Dases 1 to 145)
Lusby,E., Fife,K.H. and Berns,K.I.
avcleotide sequence of the inverted terminal repetition in adeno-associated virus DNA
J. Virol. 34 (2), 402-409 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobases 1 to 145)
Lefebvre.R.B., Riva, S. and Berns, K.I.
Conformation trakes precedence over sequence in adeno-associated virus DNA replication.
Mol. Cell. Biol. 4 (7), 1416-1419 (1984)
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100.0%; Pred. No. 1.5e-23;
iive 0; Mismatches 0;
RHONE POULENC RORER SA (FR)
Other publication AV 1822695 950918
Other publication FR 2716893 950908
Location/Qualifiers

    .145
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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TITLE

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Adeno-associated virus origin of replication (genome 3' terminus). M10681.1 GI:209626
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Adeno-associated virus 2H
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 145)
Berns, K.I., Hauswirth, W.W., Fife, K.H. and Lusby, E.
Adeno-associated virus DNA replication
Cold Spring Harb. Symp. Quant. Biol. 43 Pt 2, 781-787 (1979)
                                                                                                                                                                                                                                                                 145 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC
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                                                                                                                              Indels

    145
/organism="Adeno-associated virus 2H'
/mol type="genomic DNA"
/db_Xref="taxon:10805"

                                                                                 Query Match 100.0%; Score 145; DB 14; Best Local Similarity 100.0%; Pred. No. 1.5e-23; Matches 145; Conservative 0; Mismatches 0;
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Sequence 1 from patent US 5869305.
AR034135
AR034135.1 GI:5949740
/mol_type="genomic DNA"
/db_xref="taxon:10805"
2 bases upstream of HaeIII site.
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TITLE JOURNAL FEATURES

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Adeno-associated viruses and uses thereof
Patent: WO 0125465-A 7 12-APR-2001;
University of Iowa Research Foundation (US); Engelhardt, John (US); Dongsheng, Duan (US); Ziying, Yan (US)
Location/Quanlifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/mole="SEQ ID NO:1 of U.S. Patent No. 5,478,745"
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100.0%; Pred. No. 1.5e-23;
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Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 145; Conservative 0; Mismatches 0;
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               Unclassified.

1 (bases 1 to 165)
Engelhardt, 7.F. and Duan, D.
Adeno-associated virus vectors
Patent: US 6436392-A 7 20-AUG-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7 from Patent WO0125465.
AX106702
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    /organism="unknown"
    /mol_type="genomic DNA"

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1 (bases 1 to 165)
SamulbKi, X., and Xiao, X.
Recombinant viral vector system
Patent: US 5478745-A 1 26-DEC-1995;
Location/Qualifiers
                                   1 (bases 1 to 165)
SamulaKi, K. Jude. and Xiao, X.
Recombinant viral vector system
Patent: US 5669305-A 1 09-FEB-1999;
Location/Qualifiers
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 7 from patent US 6436392.
AR223306
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Sequence 1 from patent US 5478745.
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                                                                                                                                                                                                                                                                                                                                               Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.

(bases 1 to 2116)

Lusby,E.W. and Berns,K.I.

Mapping of the Strenini of two adeno-associated virus 2 RNAs in the left balf of the genome

J. Virol. 41 (2), 518-526 (1982)

82192580

Original source text: adeno-associated virus 2 from human hela cells.
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Repo-associated virus aav rep78 major regulatory protein, mutants
thereof and uses thereof
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2116 bp DNA linear adeno-associated virus 2 left half 45% of genome.
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1. .2116
7. Organism="Adeno-associated virus /mol_type="genomic DNA"
/db_xref="taxon:10804"
                                                                            Pred. No. 1.5e-23;
Mismatches 0;
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Sequence 5 from Patent W00132711.
AX135805 GI:14272040
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28-XAY-2002
28-XAY-209
20-WAY-1999 US 09/276625 PI
20-WAY-1998 US 60/086166,25-MAR-1999 US 09/276625 PI
F ENGELHARDT,DONGSHENG DUAN,TUYIN YANG
CI2N15/00,A01K67/027,A61K31/711,A61K48/00,C07K14/47,C12N5/10,C12N15/00,
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Engelhardt,J.F., Duan,D. and Yang,T.
Adeno-associated virus vectors and uses thereof
Patent: 197 2002515257-8 7 28-MAY-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS UNROWN
PO 197 2002515257-8/7
PD 28-MAY-1999 UP 2006549752
PR 20-MAY-1999 US 60/0861
PC C12N15/00,
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/organism='Unknown'
Location/Qualifiers
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/organia="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Procaryoric libraries and uses
Patent: WO 02066653-A 58 29-AUG-2002;
Xencor (US)
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Sequence 58 from Patent WO02066653.
AX703496
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/ COUGUID 1648.C3
/ COUGUID 16
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Patent: WO 0132711-A 5 10-MAY-2001;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
Location/Qualifiers
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Pred. No. 9.3e-24;
Mismatches 0; Indels 0
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                                                                                                                  /organism="Adeno-associated virus 2"
|mol_type="unassigned DNA"
|db_xref="taxon:10804"
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Pred. No. 9.3e-24;
; Mismatches 0;
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Cytotoxic agents
Patent: WO 0180840-A 1 01-NOV-2001;
BTG INTENATIONAL LIMITED (GB)
Location/Qualifiers
1. 4675
/organism="Adeno-associated vi: /mol_type="unassigned DNA"
/db_xref="taxon:10804"
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Sequence 1 from Patent WO0180840.
AX286292.1 GI:17048540
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tive 0;
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llarity 100.0%;
Conservative 0;
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Best Local Similarity 100.
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Best Local S:
Matches 145
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unclassified.
I (bases I to 4675)
Ueno,T., Matsumura,H., Tanaka,K., Iwasaki,T., Ueno,M., Fujinaga,K.,
Asada,K. and Kato,I.
                                                                                                                                                                                                                    PAT 23-JUN-2003
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Patent: WO 0132899-A 1 10-MAY-2001;
TAKARA SHUZO CO LID, TAKASHI UENO, HAJIME MATSUMURA, KEIJI TANAKA,
TOMOKO IWASAKI, MITSUHIRO UENO, KEI FUJINAGA, KIYOZO ASADA, IKUNOSHIN
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29-OCT-1999 JP 99P 308839
TAKASHI UENO,HAJIME MATSUMURA,KEIJI TANAKA,TOMOKO IWASAKI, PI
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                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus 2
Adeno-associated virus 2
Viruses; ssDNA viruses; Parvoviridae, Parvovirinae; Dependovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A method of defecting and/or identifying adeno-associated virus (AVV) sequences and isolating novel sequences identified thereby Patent: EP 1310571.A 7 14-MAY-2003; The Trustees of The University of Pennsylvania (US)
1 TIGGCCACTCCCTCTCTGCGCTCGCTCGCTCACGAGGCCGAGCCAACGAAGGTCGCC
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1. 4675
/organism="Adeno-associated virus 2"
/duol_type="unassigned DNA"
/db_xref="taxon:10804"
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100.0%; Pred. No. 9.3e-24;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                  AX753252 4675 bp
Sequence 7 from Patent BP1310571.
AX753252 4X753252.1 GI:32166109
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BD094552
BD094552.1 GI:22640140
WO 0132899-A/1.
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WO 0132899-A/1
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Srivastava,A., Lusby,E.W. and Berns,K.I.
Nucleotide sequence and organization of the adeno-associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Original source text: Adeno-associated virus 2 DNA from human HeLa cells.
             PI KEI FUJINAGA, KIYOZO ASADA, IKUNOSHIN KATO
PC C12N15/861,A61K35/12,A61K35/76,A61K48/00,C12N5/10,C12N7/01 CC
Method of transferring gene
                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative splicing; complete genome; major coat protein.
Adeno-associated virus 2
Adeno-associated virus 2
Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.

1 (bases 4532 to 4675)
Samulski, R.J., Strivastava, A., Berns, K.I. and Muzyczka, N.
Rescue of adeno-associated virus from recombinant plasmids: gene correction within the terminal repeats of AAV
                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                   /organism='Adeno-associated virus'.
                                                                                                                                                                                                                         DB 6; Length 4675;
                                                                                                                                                                                                                         Query Match
100.0%; Score 145; DB 6; Length 46'
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 145; Conservative 0; Mismatches 0; Indels
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/note="major coat protein A mRNA (alt.)"
join(321. .1906,2228. .2252)
/note="major coat protein A' (alt.)"
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    .4675
/organism="Adeno-associated virus
/mol_type="genomic DNA"
/mol_xref="taxon:10804"
    .145

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                                                              Location/Qualifiers
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/note="flip oriented DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/protein_id="AAA42372.1"
/db_xref="G1:209617"
                                                                                                                            1. .4675
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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MITSUHIRO UENO,
PI KEI FUJINAG;
PC CIZNIS/861,7
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TITLE
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REFERENCE
AUTHORS
TITLE
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MEDLINE
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WALPTYNHILYKQISSQSGANDNHYEGYSTFWGYFDFNRFHCHFSPDWQRLINNW
REPRRAINSPGLENIOWEWTONDGTTIANNLTSTYOVFTDSEYQLFYLGSAHQGGL
PPFPADVFWVPRYPOYGYTLLANGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTEEDVPF
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ANPSTTFSAAKFASFITQYSTGHGQRGDRVGAABGKQQTLESRNSVHFQLQQVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAGKIMSLIKTAPDYLYGQQPVEDISSNRIYKILELMGYDPQYAASVFLGWATKKFGK
RNTIWLFGPATTGKTNIABALAHYVPFYGCVNWTNENFPRDCVDKGVIWWEGKMTA
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TQPELGWAWTNWEGYLSACLINLTERKRIVAQHLTHVSGTGGCNKCWDECYIPVLLPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA42375.1"
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KVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFEHQQPLQ
DRMFKFELTRRLDHDFGKVTKQEVKDFRWAKDHVVEVEHEFYVKKGGAKKRPAPSDA
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ICPTHGQKDCLECFPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACTACDLVNVDLDD
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/translation="MATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCLECFPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACTACDLVNVDLDDCIFEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       873. .4447

horte="major coat protein A mRNA (alt.)"

join(993. .1906,2228. .2252)

/note="major coat protein Aa (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1853. .4447
/note="major coat protein B mRNA (alt.)"
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/note="major coat protein A'' (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4531. .4675
/note="3' inverted terminal repeat"
4592. .4634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1907. .2227
/note="major coat protein A intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2810. 4324
/note="major coat protein B"
                                                                                                                                                                                                                                                                                                                                                      321. .2186
/note="major coat protein A"
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		0;
		Gaps
	4675;	0
	Length	Indels 0; Gaps (
	DB 14;	;0
/note="flop oriented DNA" genomic DNA.	Query Match 100.0%; Score 145; DB 14; Length 4675; Best Local Similarity 100.0%; Pred. No. 9.3e-24;	vative 0; Mismatches
/note="flop o	h Similarity	fatches 145; Conservative
ORIGIN	Query Matc Best Local	Matches 1

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	0; Gaps	GTCGCC	<u>=</u>	ししせし上せ
	0	CAAAG	<u>=</u>	54447
ì	Indels	CCGGGCGAC	= = =	こるさしさささして
-24;	0;	TGAGG	Ξ	びけるひと
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